



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 95546

TO: Jeffrey Parkin
Location: CM1 8E15
Art Unit: 1648
Thursday, June 05, 2003
OS / CR
Case Serial Number: 605573

From: Alex Waclawiw
Location: Biotech-Chem Library
CM1-6A02
Phone: 308-4491

Alexandra.waclawiw@uspto.gov

Search Notes

Examiner Parkin,

I was not able to remove the inventor's name from the compugen search. The program does not allow for that option.

I also searched the sequence on STN. There were no sequences with less than 20 amino acids. I printed out hits with sequence length between 20-30 amino acids just in case this information would be useful. The reference for these sequences was the inventor's work

Alexandra Waclawiw

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STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact:*

Mary Hale, Information Branch Supervisor
308-4258, CM1-1E01

Voluntary Results Feedback Form

➤ *I am an examiner in Workgroup:* *Example: 1610*

➤ *Relevant prior art found, search results used as follows:*

- 102 rejection
- 103 rejection
- Cited as being of interest.
- Helped examiner better understand the invention.
- Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- Foreign Patent(s)
- Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ *Relevant prior art not found:*

- Results verified the lack of relevant prior art (helped determine patentability).
- Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library CM1 – Circ. Desk

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Parkin 09/605,573

=>d his

(FILE 'HOME' ENTERED AT 10:54:21 ON 05 JUN 2003)

FILE 'REGISTRY' ENTERED AT 10:55:14 ON 05 JUN 2003

L1 16 S LNSWGCKGRIICYTS/SQSP

L2 0 S L1 AND SQL<21

L3 0 S L1 AND SQL=20

L4 9 S L1 AND SQL<31

FILE 'HCAPLUS' ENTERED AT 10:58:23 ON 05 JUN 2003

L5 1 S L4

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=> fil reg
FILE 'REGISTRY' ENTERED AT 10:58:51 ON 05 JUN 2003
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
COPYRIGHT (C) 2003 American Chemical Society (ACS)

Property values tagged with IC are from the ZIC/VINITI data file
provided by InfoChem.

STRUCTURE FILE UPDATES: 4 JUN 2003 HIGHEST RN 525536-93-0
DICTIONARY FILE UPDATES: 4 JUN 2003 HIGHEST RN 525536-93-0

TSCA INFORMATION NOW CURRENT THROUGH JANUARY 6, 2003

Please note that search-term pricing does apply when
conducting SmartSELECT searches.

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. See HELP
PROPERTIES for more information. See STNote 27, Searching Properties
in the CAS Registry File, for complete details:
<http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf>

=> d que 14
L1 16 SEA FILE=REGISTRY ABB=ON PLU=ON LNSWGCKGRIICYTS/SQSP
L4 9 SEA FILE=REGISTRY ABB=ON PLU=ON L1 AND SQL<31

=> d sqide3 14 1-9

L4 ANSWER 1 OF 9 REGISTRY COPYRIGHT 2003 ACS
RN 276694-91-8 REGISTRY
CN L-Histidine, glycyl-L-arginyl-L-.alpha.-glutamyl-L-threonyl-L-leucyl-L-methionyl-L-glutaminylglycyl-L-glutaminyl-L-glutaminyl-L-phenylalanyl-L-leucyl-L-asparaginyl-L-seryl-L-tryptophylglycyl-L-cysteinyl-L-lysylglycyl-L-arginyl-L-isoleucyl-L-isoleucyl-L-cysteinyl-L-tyrosyl-L-threonyl-L-seryl-L-alanyl-L-arginyl-L-tryptophyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 4: PN: JP2000157268 PAGE: 37 claimed sequence
FS PROTEIN SEQUENCE; STEREOSEARCH
SQL 30

PATENT ANNOTATIONS (PNTE):

Sequence	Patent
Source	Reference
=====	
Not Given	JP2000157268
	claimed PAGE
	37

SEQ3 1 Gly-Arg-Glu-Thr-Leu-Met-Gln-Gly-Gln-Gln-
11 Phe-Leu-Asn-Ser-Trp-Gly-Cys-Lys-Gly-Arg-
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21 Ile-Ile-Cys-Tyr-Thr-Ser-Ala-Arg-Trp-His
=====
HITS AT: 12-26

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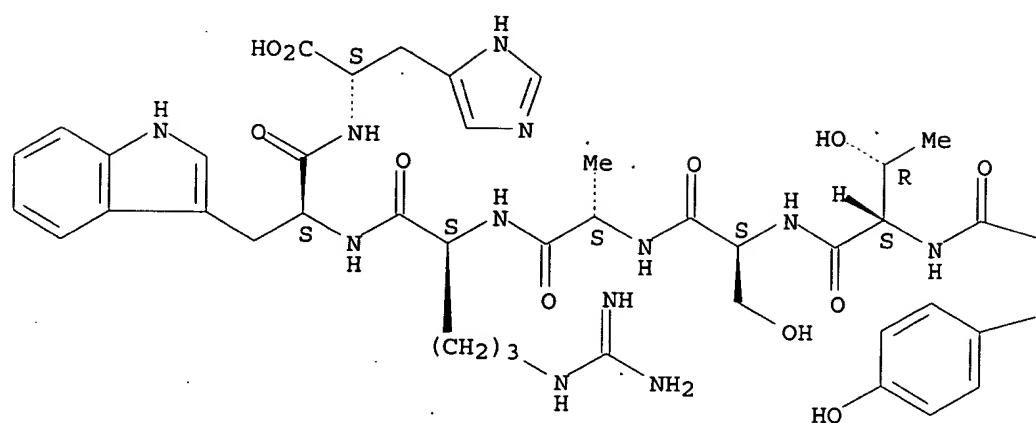
MF C154 H236 N48 O42 S3

SR

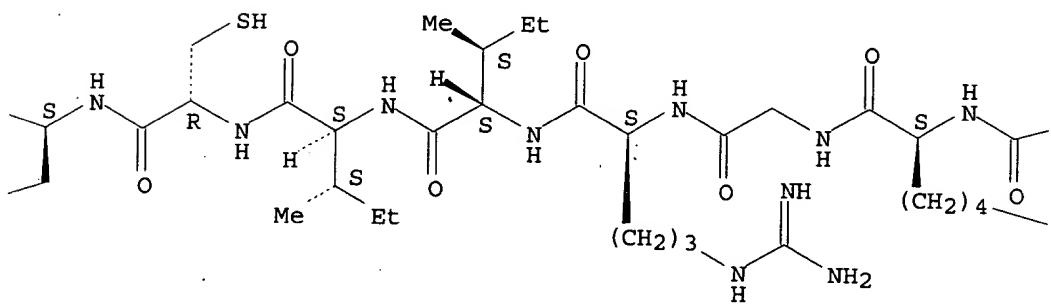
LC STN Files: CA, CAPIUS, USPATELL

Absolute stereochemistry.

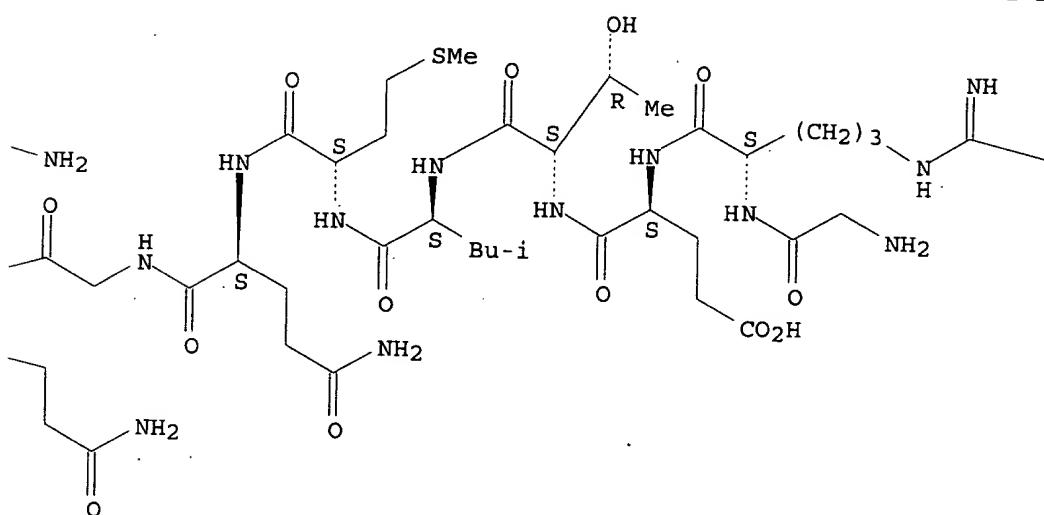
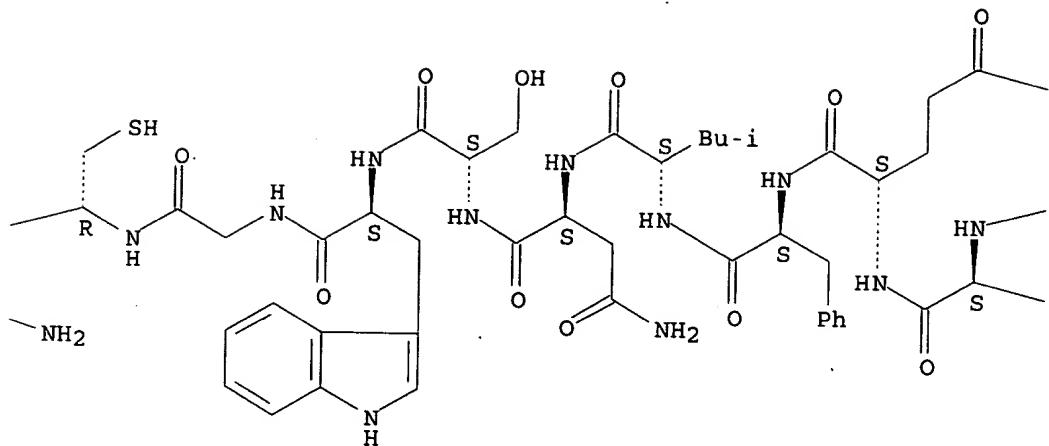
PAGE 1-A



PAGE 1-B



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1 REFERENCES IN FILE CA (1957 TO DATE)
 1 REFERENCES IN FILE CAPLUS (1957 TO DATE)

L4 ANSWER 2 OF 9 REGISTRY COPYRIGHT 2003 ACS
 RN 276687-01-5 REGISTRY
 CN Peptide, (Glu-Thr-Leu-Met-Gln-Xaa-Gln-Gln-Arg-Leu-Asn-Ser-Trp-Gly-Cys-Lys-Gly-Arg-Ile-Ile-Cys-Tyr-Thr-Ser-Ala-Arg-Trp-His) (9CI) (CA INDEX NAME)
 OTHER NAMES:
 CN 6: PN: JP2000157268 PAGE: 37 claimed sequence
 FS PROTEIN SEQUENCE
 SQL 28
 NTE

type	location	description
uncommon	Aaa-6	-

PATENT ANNOTATIONS (PNTE):

Sequence	Patent
Source	Reference
Not Given	JP2000157268
	claimed PAGE
	37

SEQ3 1 Glu-Thr-Leu-Met-Gln-Aaa-Gln-Gln-Arg-Leu-
 11 Asn-Ser-Trp-Gly-Cys-Lys-Gly-Arg-Ile-Ile-
 21 Cys-Tyr-Thr-Ser-Ala-Arg-Trp-His
 HITS AT: 10-24

RELATED SEQUENCES AVAILABLE WITH SEQLINK

MF Unspecified
 CI MAN
 SR CA
 LC STN Files: CA, CAPLUS, USPATFULL
 1 REFERENCES IN FILE CA (1957 TO DATE)
 1 REFERENCES IN FILE CAPLUS (1957 TO DATE)

L4 ANSWER 3 OF 9 REGISTRY COPYRIGHT 2003 ACS
 RN 276687-00-4 REGISTRY
 CN Peptide, (Xaa-Gln-Gln-Arg-Leu-Asn-Ser-Trp-Gly-Cys-Lys-Gly-Arg-Ile-Ile-Cys-Tyr-Thr-Ser-Ala-Arg-Trp-His) (9CI) (CA INDEX NAME)
 OTHER NAMES:
 CN 5: PN: JP2000157268 PAGE: 37 claimed sequence
 FS PROTEIN SEQUENCE
 SQL 23
 NTE

type	location	description
uncommon	Aaa-1	-

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L4 ANSWER 5 OF 9 REGISTRY COPYRIGHT 2003 ACS
 RN 276250-48-7 REGISTRY
 CN 3: PN: JP2000157268 SEQID: 62 unclaimed protein (9CI) (CA INDEX NAME)
 FS PROTEIN SEQUENCE
 SQL 28
 NTE

type	location	description
uncommon	Aaa-6	

PATENT ANNOTATIONS (PNTE) :

Sequence	Patent
Source	Reference

Not Given	JP2000157268
	unclaimed
	SEQID 62

SEQ3 1 Glu-Thr-Leu-Met-Gln-Aaa-Gln-Gln-Arg-Leu-
 11 Asn-Ser-Trp-Gly-Cys-Lys-Gly-Arg-Arg-Ile-Ile-
 21 Cys-Tyr-Thr-Ser-Ala-Arg-Trp-His

HITS AT: 10-24

RELATED SEQUENCES AVAILABLE WITH SEQLINK

MF Unspecified
 CI MAN
 SR CA
 LC STN Files: CA, CAPLUS, USPATFULL
 1 REFERENCES IN FILE CA (1957 TO DATE)
 1 REFERENCES IN FILE CAPLUS (1957 TO DATE)

L4 ANSWER 6 OF 9 REGISTRY COPYRIGHT 2003 ACS
 RN 276250-47-6 REGISTRY
 CN 2: PN: JP2000157268 SEQID: 60 unclaimed protein (9CI) (CA INDEX NAME)
 FS PROTEIN SEQUENCE
 SQL 23
 NTE

type	location	description
uncommon	Aaa-1	

PATENT ANNOTATIONS (PNTE) :

Sequence	Patent
Source	Reference

Not Given	JP2000157268
	unclaimed
	SEQID 60

SEQ3 1 Aaa-Gln-Gln-Arg-Leu-Asn-Ser-Trp-Gly-Cys-

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=====
 11 Lys-Gly-Arg-Ile-Ile-Cys-Tyr-Thr-Ser-Ala-
 =====
 21 Arg-Trp-His

HITS AT: 5-19

RELATED SEQUENCES AVAILABLE WITH SEQLINK

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, USPATFULL

1 REFERENCES IN FILE CA (1957 TO DATE)
 1 REFERENCES IN FILE CAPLUS (1957 TO DATE)

L4 ANSWER 7 OF 9 REGISTRY COPYRIGHT 2003 ACS

RN 275801-53-1 REGISTRY

CN 135: PN: JP2000157268 SEQID: 69 unclaimed sequence (9CI) (CA INDEX NAME)

FS PROTEIN SEQUENCE; STEREOSEARCH

SQL 30

PATENT ANNOTATIONS (PNTE) :

Sequence | Patent

Source | Reference

=====+=====

Not Given	JP2000157268
	unclaimed
	SEQID 69

SEQ3 1 Gly-Arg-Glu-Thr-Leu-Met-Gln-Asp-Gln-Gln-
 11 Arg-Leu-Asn-Ser-Trp-Gly-Cys-Lys-Gly-Arg-
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HITS AT: 12-26

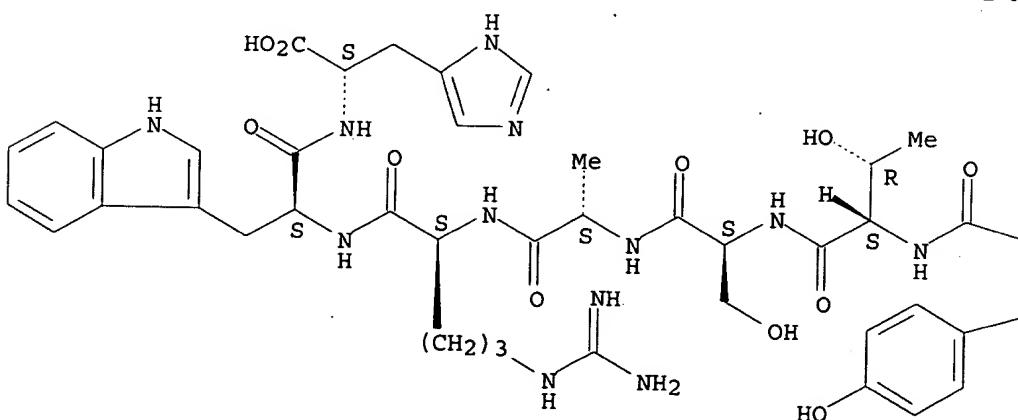
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SR CA

LC STN Files: CA, CAPLUS, USPATFULL

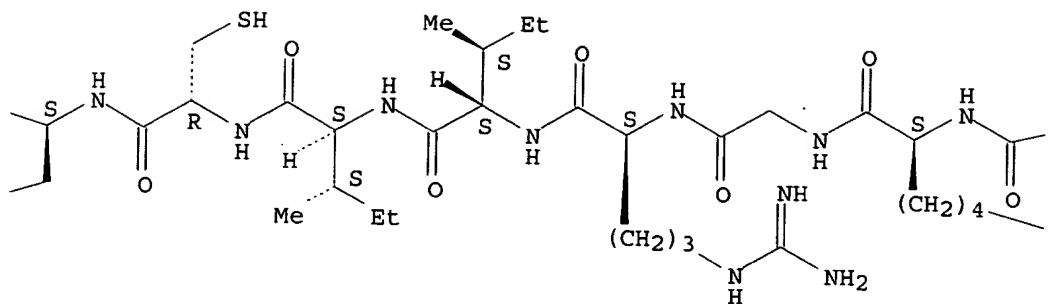
Absolute stereochemistry.

PAGE 1-A

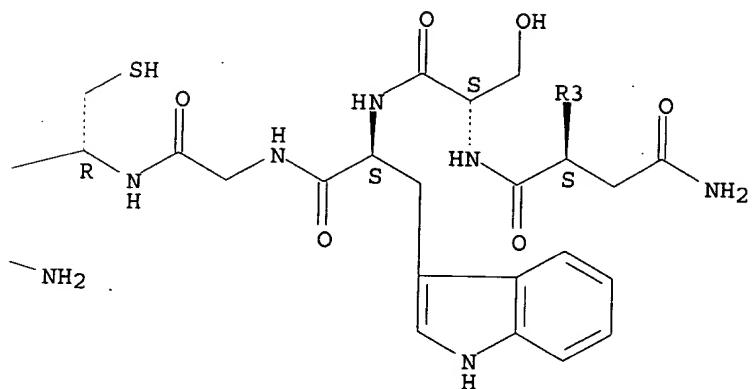


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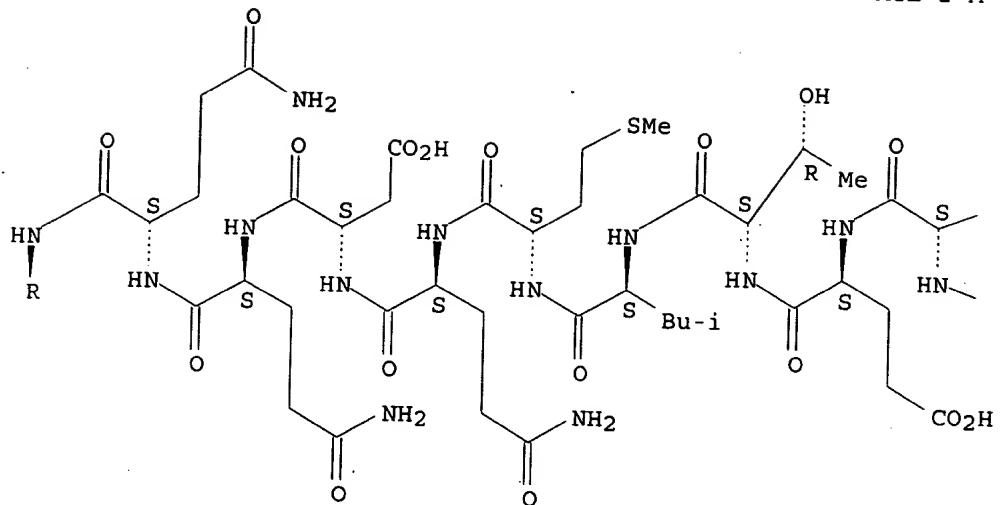


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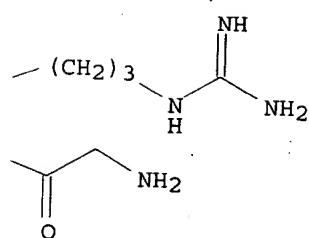


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PAGE 2-A

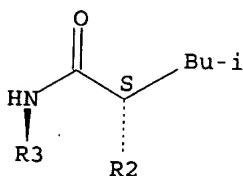
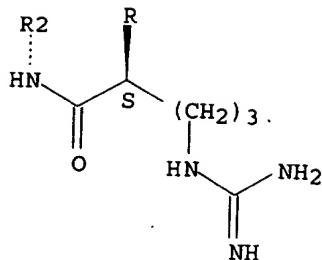


PAGE 2-B



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PAGE 3-A



1 REFERENCES IN FILE CA (1957 TO DATE)
 1 REFERENCES IN FILE CAPLUS (1957 TO DATE)

L4 ANSWER 8 OF 9 REGISTRY COPYRIGHT 2003 ACS
 RN 275801-51-9 REGISTRY
 CN L-Histidine, L-.alpha.-glutamyl-L-glutaminyl-L-glutaminyl-L-arginyl-L-leucyl-L-asparaginyl-L-seryl-L-tryptophylglycyl-L-cysteinyl-L-lysylglycyl-L-arginyl-L-isoleucyl-L-isoleucyl-L-cysteinyl-L-tyrosyl-L-threonyl-L-seryl-L-alanyl-L-arginyl-L-tryptophyl- (9CI) (CA INDEX NAME)
 OTHER NAMES:
 CN 127: PN: JP2000157268 SEQID: 61 unclaimed sequence
 FS PROTEIN SEQUENCE; STEREOSEARCH
 SQL 23

PATENT ANNOTATIONS (PNTE):

Sequence	Patent
Source	Reference
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Not Given	JP2000157268
	unclaimed
	SEQID 61

SEQ3 1 Glu-Gln-Gln-Arg-Leu-Asn-Ser-Trp-Gly-Cys-
 11 Lys-Gly-Arg-Ile-Ile-Cys-Tyr-Thr-Ser-Ala-
 21 Arg-Trp-His

HITS AT: 5-19

MF C121 H186 N40 O33 S2

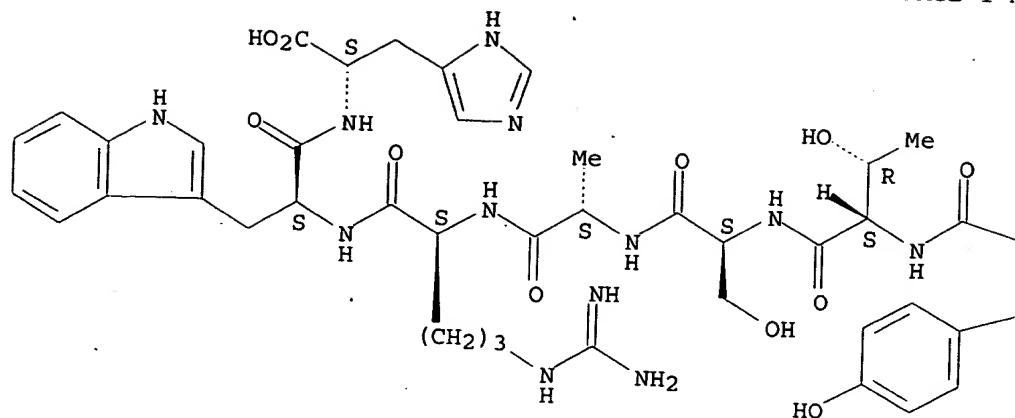
SR CA

LC STN Files: CA, CAPLUS, USPATFULL

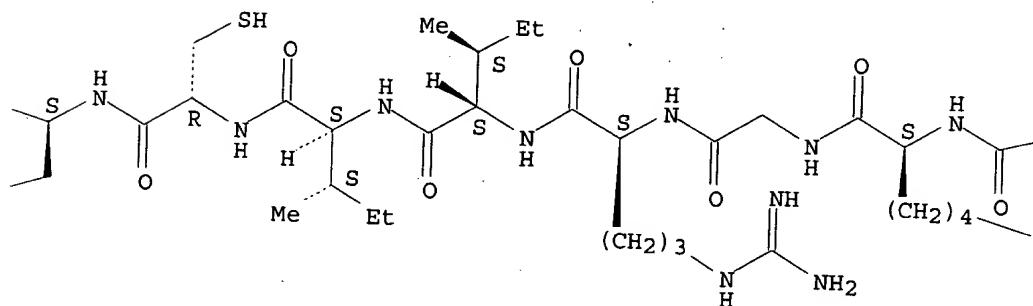
Absolute stereochemistry.

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PAGE 1-A

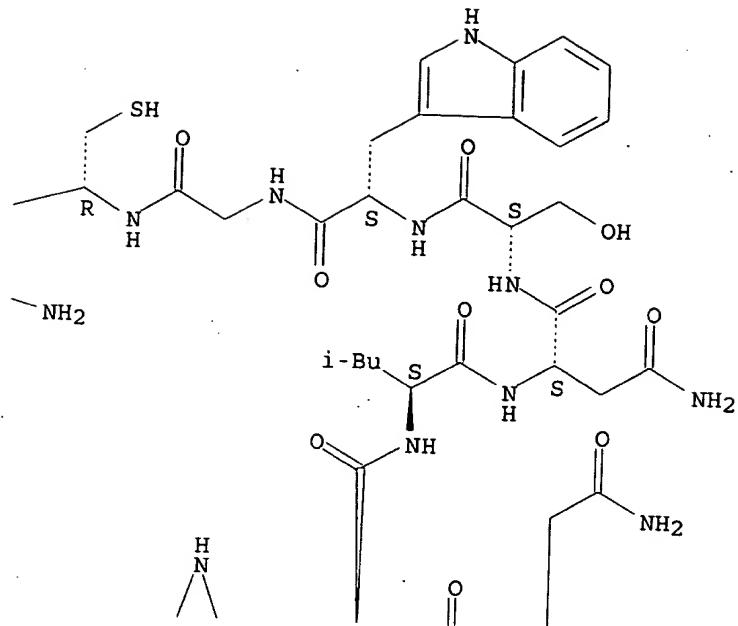


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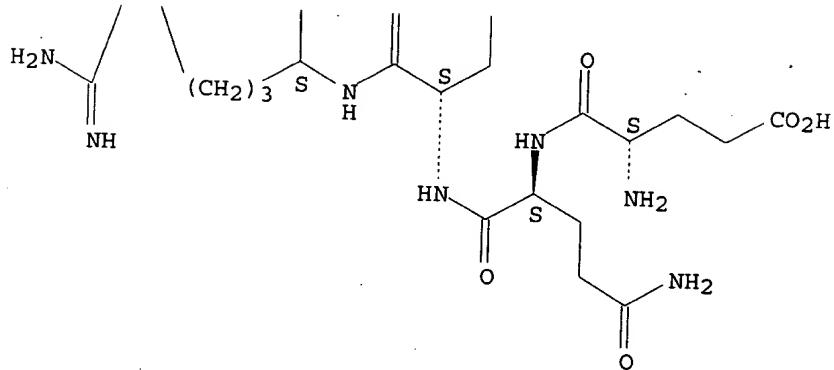


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PAGE 1-C



PAGE 2-C



1 REFERENCES IN FILE CA (1957 TO DATE)
 1 REFERENCES IN FILE CAPLUS (1957 TO DATE)

L4 ANSWER 9 OF 9 REGISTRY COPYRIGHT 2003 ACS
 RN 275801-47-3 REGISTRY
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 OTHER NAMES:
 CN 125: PN: JP2000157268 SEQID: 59 unclaimed sequence
 FS PROTEIN SEQUENCE; STEREOSEARCH
 SQL 23

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PATENT ANNOTATIONS (PNTE):

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	unclaimed
	SEQID 59

SEQ3 1 Asn-Gln-Gln-Arg-Leu-Asn-Ser-Trp-Gly-Cys-
 11 Lys-Gly-Arg-Ile-Ile-Cys-Tyr-Thr-Ser-Ala-
 21 Arg-Trp-His

HITS AT: 5-19

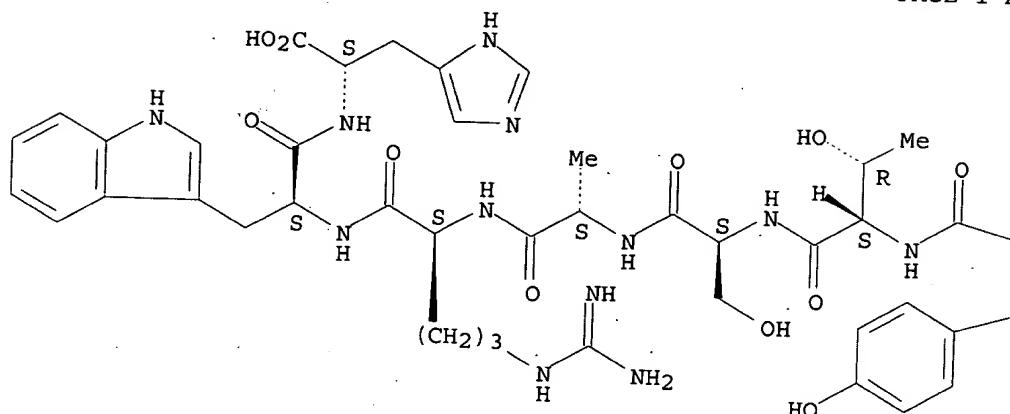
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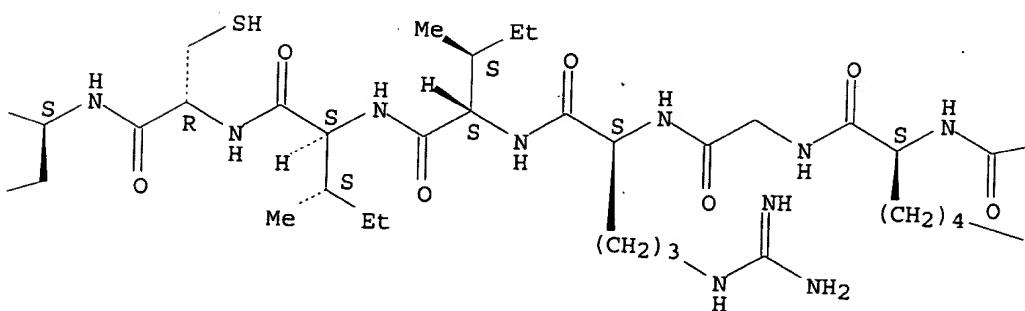
LC STN Files: CA, CAPLUS, USPATFULL

Absolute stereochemistry.

PAGE 1-A

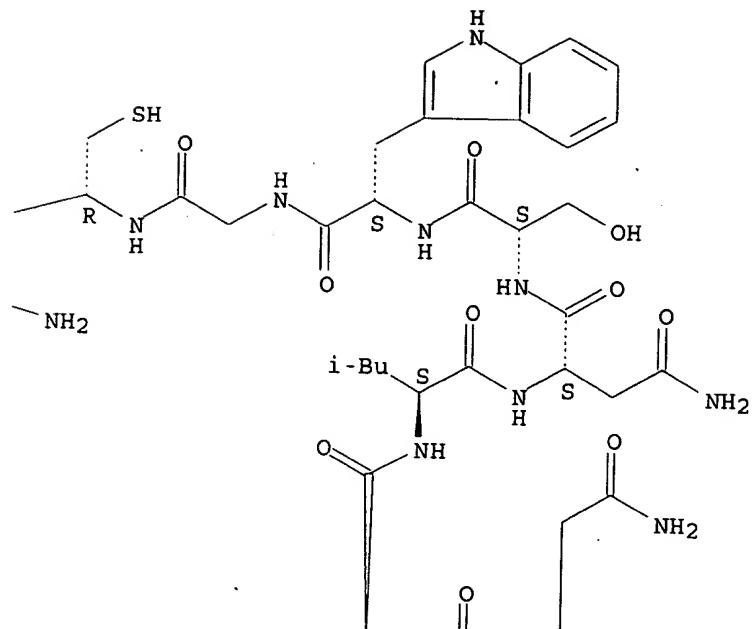


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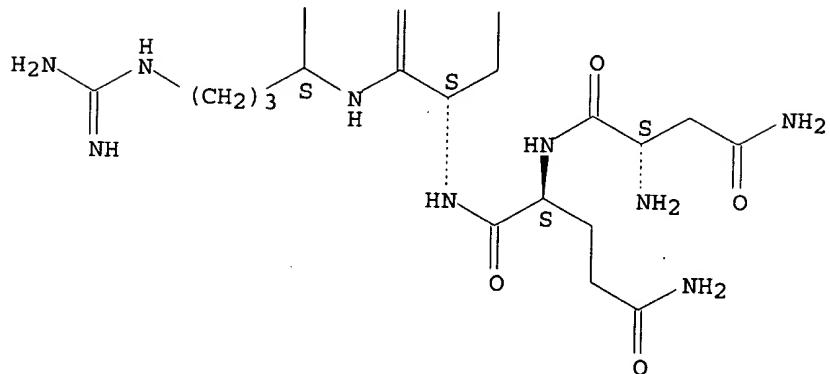


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PAGE 1-C



PAGE 2-C



1 REFERENCES IN FILE CA (1957 TO DATE)
1 REFERENCES IN FILE CAPLUS (1957 TO DATE)

=> fil hcaplus
FILE 'HCAPLUS' ENTERED AT 10:59:08 ON 05 JUN 2003
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FILE COVERS 1907 - 5 Jun 2003 VOL 138 ISS 23
FILE LAST UPDATED: 4 Jun 2003 (20030604/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

'OBI' IS DEFAULT SEARCH FIELD FOR 'HCAPLUS' FILE

=> d que nos 15

L1 16 SEA FILE=REGISTRY ABB=ON PLU=ON LNSWGCKGRIICYTS/SQSP
L4 9 SEA FILE=REGISTRY ABB=ON PLU=ON L1 AND SQL<31
L5 1 SEA FILE=HCAPLUS ABB=ON PLU=ON L4

=> d .ca 15

L5 ANSWER 1 OF 1 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:392837 HCAPLUS
DOCUMENT NUMBER: 133:55969
TITLE: Peptide for detection of Group O HIV-1 and use for diagnosis
INVENTOR(S): Deleys, Robert; Chen, Jan
PATENT ASSIGNEE(S): Ortho-Clinical Diagnostics, Inc., USA
SOURCE: Jpn. Kokai Tokkyo Koho, 103 pp.
CODEN: JKXXAF
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
JP 2000157268	A2	20000613	JP 1999-338385	19991129
US 6149910	A	20001121	US 1999-433428	19991104
EP 1013766	A2	20000628	EP 1999-309491	19991129
EP 1013766	A3	20030129		

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
IE, SI, LT, LV, FI, RO

PRIORITY APPLN. INFO.: US 1998-110292P P 19981130
US 1999-119138P P 19990208
US 1999-433428 A 19991104

AB Disclosed are the peptides derived from the immunodominant region of the Group O HIV-1 gp41 envelope protein, which do not correspond to any known naturally occurring Group O sequence or variant. The peptides bind to the antibodies to Group O HIV-1. The peptides are useful in detecting antibodies arise from the infection by Group O HIV-1. The peptides may be prep'd. in a hybrid form with that of Group M HIV-1.

IC ICM C12N015-00
ICS C07K014-16; C07K016-12; C12N001-15; C12N001-19; C12N001-21;
C12N005-10; C12P021-02; G01N033-569; C12P021-08

CC 10-1 (Microbial, Algal, and Fungal Biochemistry)

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Section cross-reference(s): 14
IT 276687-00-4 276687-01-5 276694-91-8
276873-37-1
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified);
THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study);
USES (Uses)
(antibody to Group O HIV-1 detection by; peptide for detection of Group
O HIV-1 and use for diagnosis)
IT 275389-20-3 275389-22-5 275829-31-7 276250-39-6 276250-40-9
276250-41-0 276250-42-1 276250-43-2 276250-47-6
276250-48-7 276250-49-8 276250-50-1 276873-73-5
RL: PRP (Properties)
(unclaimed protein sequence; peptide for detection of Group O HIV-1 and
use for diagnosis)
IT 173145-89-6 275389-13-4 275389-14-5 275389-15-6 275389-16-7
275389-17-8 275389-18-9 275389-19-0 275801-47-3
275801-51-9 275801-52-0 275801-53-1 275829-37-3
276249-52-6 276249-53-7 276249-62-8 276249-72-0 276249-78-6
276249-79-7 276249-80-0 276249-81-1 276249-82-2 276249-83-3
276249-84-4 276249-86-6 276249-87-7 276249-88-8 276249-90-2
276249-91-3 276249-92-4 276249-93-5 276249-95-7 276249-96-8
276249-97-9 276249-98-0 276249-99-1 276250-00-1 276250-01-2
276250-02-3 276250-03-4 276250-04-5 276250-25-0 276250-26-1
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276250-32-9 276250-33-0 276250-34-1 276250-35-2 276250-36-3
RL: PRP (Properties)
(unclaimed sequence; peptide for detection of Group O HIV-1 and use for
diagnosis)

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

June 5, 2003, 07:21:32 ;

Search time 13 Seconds

(without alignments)

33.950 Million cell updates/sec

Title:

US-09-605-573a-69_COPY_12-26

Sequence:

1 LNSWGCKGRICIVTS 15

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

262574 seqs, 29422922 residues

Perfect score:

. 89

Total number of hits satisfying chosen parameters:

136623

Minimum DB seq length:

0

Maximum DB seq length:

21

Post-processing:

Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Issued Patents AA:*

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 3: /ccn2_6/ptodata/1/1aa5/6A_COMBO.pep:*
 4: /ccn2_5/ptodata/1/1aa6/B_COMBO.pep:*
 5: /ccn2_6/ptodata/1/1aa6/PCUTUS_COMBO.pep:*
 6: /ccn2_6/ptodata/1/1aa6/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	72	80.9	15	1	US-08-615-219-8
2	72	80.9	15	1	US-08-615-219-29
3	68	76.4	19	1	US-08-722-597A-4
4	68	76.4	19	1	US-08-837-732-4
5	63	70.8	19	1	US-08-72-597A-3
6	63	70.8	19	1	US-08-837-732-3
7	59	66.3	19	1	US-08-472-597A-2
8	59	66.3	19	1	US-08-837-732-2
9	56	62.9	14	4	US-08-682-791B-7
10	56	62.9	14	4	US-08-682-791B-8
11	55	61.8	16	1	US-08-682-791B-11
12	55	61.8	16	1	US-08-615-279-27
13	55	61.8	16	2	US-08-765-452-7
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17	54	60.7	15	1	US-08-723-425A-5
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22	53	59.6	12	4	US-08-723-425A-177
23	53	59.6	12	4	US-08-112-206-176
24	53	59.6	12	4	US-08-682-791B-1
25	53	59.6	19	1	US-07-901-874B-14
26	53	59.6	19	1	US-08-457-865-14
27	53	59.6	20	1	US-07-633-964-14

28	53	59.6	20	1	US-08-386-956-14	Sequence 14, Appl
29	53	59.6	20	3	US-09-108-709-45	Sequence 45, Appl
30	53	59.6	21	2	US-08-16-028-2	Sequence 2, Appl
31	53	59.6	21	4	US-08-723-425A-2	Sequence 2, Appl
32	53	59.6	21	4	US-09-112-206-2	Sequence 2, Appl
33	51	57.3	12	1	US-07-633-964-2	Sequence 2, Appl
34	51	57.3	12	1	US-07-633-964-28	Sequence 2, Appl
35	51	57.3	12	1	US-07-633-964-29	Sequence 29, Appl
36	51	57.3	12	1	US-08-218-025A-121	Sequence 121, Appl
37	51	57.3	12	1	US-08-386-956-2	Sequence 2, Appl
38	51	57.3	12	1	US-08-386-956-28	Sequence 28, Appl
39	51	57.3	12	1	US-08-386-956-29	Sequence 29, Appl
40	51	57.3	12	1	US-09-108-709-2	Sequence 17, Appl
41	51	57.3	12	3	US-08-776-949-27	Sequence 27, Appl
42	51	57.3	13	3	US-09-108-709-19	Sequence 18, Appl
43	51	57.3	13	3	US-09-108-709-19	Sequence 19, Appl
44	51	57.3	14	3	US-09-108-709-20	Sequence 20, Appl
45	51	57.3	12	1	US-08-386-956-4	Sequence 4, Appl
46	50	56.2	12	1	US-08-386-956-4	Sequence 5, Appl
47	50	56.2	12	3	US-09-108-709-25	Sequence 25, Appl
48	50	56.2	13	3	US-09-108-709-25	Sequence 26, Appl
49	50	56.2	13	3	US-09-108-709-27	Sequence 27, Appl
50	50	56.2	14	3	US-09-108-709-28	Sequence 28, Appl
51	50	56.2	14	4	US-08-682-791B-3	Sequence 29, Appl
52	50	56.2	14	4	US-08-682-791B-9	Sequence 30, Appl
53	50	56.2	15	1	US-07-901-874B-16	Sequence 31, Appl
54	50	56.2	16	1	US-08-457-865-16	Sequence 32, Appl
55	50	56.2	18	6	5439792-3	Sequence 33, Appl
56	50	56.2	20	9	5439792-8	Sequence 34, Appl
57	50	56.2	20	9	5439792-9	Sequence 35, Appl
58	49	55.1	9	3	US-09-108-709-23	Sequence 36, Appl
59	49	55.1	10	2	US-08-737-0854-10	Sequence 37, Appl
60	49	55.1	10	3	US-09-108-709-22	Sequence 38, Appl
61	49	55.1	10	3	US-09-246-258-10	Sequence 39, Appl
62	49	55.1	10	4	US-09-532-106-10	Sequence 40, Appl
63	49	55.1	10	4	US-09-839-656-10	Sequence 41, Appl
64	49	55.1	11	3	US-09-108-709-21	Sequence 42, Appl
65	49	55.1	12	2	US-08-146-028-176	Sequence 43, Appl
66	49	55.1	12	2	US-08-146-028-177	Sequence 44, Appl
67	49	55.1	12	4	US-08-723-425A-177	Sequence 45, Appl
68	49	55.1	12	4	US-08-206-176	Sequence 46, Appl
69	49	55.1	12	4	US-09-112-206-177	Sequence 47, Appl
70	49	55.1	12	4	US-09-112-206-177	Sequence 48, Appl
71	48	53.9	13	4	US-08-682-791B-1	Sequence 49, Appl
72	48	53.9	14	4	US-08-682-791B-1	Sequence 50, Appl
73	47	52.8	12	1	US-07-33-954-3	Sequence 51, Appl
74	47	52.8	12	1	US-07-33-954-3	Sequence 52, Appl
75	47	52.8	12	3	US-09-108-709-34	Sequence 53, Appl
76	47	52.8	13	3	US-09-108-709-35	Sequence 54, Appl
77	47	52.8	13	3	US-09-108-709-36	Sequence 55, Appl
78	47	52.8	14	3	US-09-108-709-37	Sequence 56, Appl
79	46	51.7	11	3	US-09-108-709-29	Sequence 57, Appl
80	46	51.7	14	4	US-08-791B-10	Sequence 58, Appl
81	45	50.6	12	2	US-08-146-028-24	Sequence 59, Appl
82	45	50.6	12	4	US-08-23-425A-24	Sequence 60, Appl
83	45	50.6	12	4	US-09-112-206-24	Sequence 61, Appl
84	44	49.4	12	3	US-08-776-949-29	Sequence 62, Appl
85	43	48.3	11	3	US-09-108-709-38	Sequence 63, Appl
86	43	48.3	13	3	US-09-108-709-38	Sequence 64, Appl
87	42	47.8	13	3	US-09-108-709-28	Sequence 65, Appl
88	42	47.2	15	1	US-07-633-964-9	Sequence 66, Appl
89	42	47.2	15	1	US-08-386-956-9	Sequence 67, Appl
90	42	47.2	17	1	US-07-633-964-13	Sequence 68, Appl
91	42	47.2	17	1	US-08-386-956-5	Sequence 69, Appl
92	42	47.2	17	2	US-08-833-546-1	Sequence 70, Appl
93	42	47.2	17	3	US-09-108-709-6	Sequence 71, Appl
94	42	47.2	17	4	US-09-388-954-1	Sequence 72, Appl
95	42	47.2	19	2	US-08-655-552-8	Sequence 73, Appl
96	41	46.1	10	1	US-07-633-964-21	Sequence 74, Appl
97	41	46.1	10	1	US-08-386-956-21	Sequence 75, Appl
98	41	46.1	10	3	US-09-108-709-16	Sequence 76, Appl
99	41	46.1	14	4	US-08-682-791B-4	Sequence 77, Appl
100	41	46.1	14	4	US-08-682-791B-6	Sequence 78, Appl

ALIGNMENTS

APPLICANT: SEIDEL, Christoph
APPLICANT: WIENHUES, Ursula-Henrike
APPLICANT: FAATZ, Elke
APPLICANT: SCHMITT, Urban
TITLE OF INVENTION: HAPten-LABELLED PEPTIDES

RESULT 1

US-08-615-279-8

Sequence 8, Application US/08615279

Patent No. 5804371

GENERAL INFORMATION:

APPLICANT: H SS, Eva

APPLICANT: SEIDEL, Christoph

APPLICANT: WIENHUES, Ursula-Henrike

APPLICANT: FAATZ, Elke

APPLICANT: SCHMITT, Urban

TITLE OF INVENTION: HAPten-LABELLED PEPTIDES

NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIKAIDO, MARTELSTEIN, MURRAY & ORAM LLP

STREET: 655 Fifteenth Street, N. W., Suite 330 - G

STREET: Street Lobby

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-5701

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/615,279

FILING DATE: 25-MAR-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP95/02921

FILING DATE: 24-JUL-1995

ATTORNEY/AGENT INFORMATION:

NAME: BERMAN, Richard J.

REGISTRATION NUMBER: 39,107

REFERENCE/DOCKET NUMBER: P564-6006

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202/638-5000

TELEFAX: 202/638-4810

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: Linear

MOLECULE TYPE: Protein

FEATURE:

NAME/KEY: Modified-site

LOCATION: 1

OTHER INFORMATION: /note=

"digoxigenin-3-cme-beta-alanine-epsilon-aminocaproic acid-beta-alanine is attached to the Leu at the 1 position

US-08-615-279-29

Query Match 80.9%; Score 72; DB 1; Length 15;

Best Local Similarity 66.7%; Pred. No. 7.9e-05; 1; Indels 0; Gaps 0;

Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNSWGCKGRILYTS 15

Db 1 LSIWGCKKLVCTS 15

RESULT 3

US-08-472-597A-4

Sequence 4, Application US/08472597A

Patent No. 5624797

GENERAL INFORMATION:

APPLICANT: Bridon, D. P.

APPLICANT: Sze, I.S.Y.

APPLICANT: Daghfal, D.J.

APPLICANT: Jaffe, K.D.

APPLICANT: Colpitts, T.L.

TITLE OF INVENTION: Peptides for HIV-1 Detection

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: ABBOTT LABORATORIES

STREET: ONE HUNDRED ABBOTT PARK ROAD

CITY: ABBOTT PARK

RESULT 2

US-08-615-279-29

Query Match 80.9%; Score 72; DB 1; Length 15;

Best Local Similarity 66.7%; Pred. No. 7.9e-05; 1; Indels 0; Gaps 0;

Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNSWGCKGRILYTS 15

Db 1 LSIWGCKKLVCTS 15

RESULT 3

US-08-472-597A-4

Sequence 4, Application US/08472597A

Patent No. 5624797

GENERAL INFORMATION:

APPLICANT: Bridon, D. P.

APPLICANT: Sze, I.S.Y.

APPLICANT: Daghfal, D.J.

APPLICANT: Jaffe, K.D.

APPLICANT: Colpitts, T.L.

TITLE OF INVENTION: Peptides for HIV-1 Detection

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: ABBOTT LABORATORIES

STREET: ONE HUNDRED ABBOTT PARK ROAD

CITY: ABBOTT PARK

COUNTRY: USA
 STATE: IL
 ZIP: 60064-3500
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/472,597A
 FILING DATE: 08/08/1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: POREMSKI, PRISCILLA E.
 REGISTRATION NUMBER: 33,207
 REFERENCE/DOCKET NUMBER: 5765.US.01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 708-937-6365
 TELEFAX: 708-938-2623
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-837-732-4
 Query Match 76.4%; Score 68; DB 1; Length 19;
 Best Local Similarity 71.4%; Pred. No. 0.00039; Matches 10; Conservative 10; Length: 19; Pred. No. 0.00039; Mismatches 2; Indels 0; Gaps 0;
 Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 1 LNSWGCKGRICYT 14
 | ||||:|||
 6 LGIWCCKKLICYT 19
 SUIT 4
 -08-837-732-4
 Sequence 4, Application US/08837732
 PATENT NO. 580983
 GENERAL INFORMATION:
 APPLICANT: Bridon, D.P.
 APPLICANT: Sze, I.S.Y.
 APPLICANT: Dagħfal, D.J.
 APPLICANT: Jaffe, K.D.
 APPLICANT: Colpitts, T.L.
 TITLE OF INVENTION: Peptides for HIV-1 Detection
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ABBOTT LABORATORIES
 STREET: ONE HUNDRED ABBOTT PARK ROAD
 CITY: ABBOTT PARK
 STATE: IL
 COUNTRY: USA
 ZIP: 60064-3500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/472,597A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: POREMSKI, PRISCILLA E.
 REGISTRATION NUMBER: 33,207
 REFERENCE/DOCKET NUMBER: 5765.US.01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 708-937-6365
 TELEFAX: 708-938-2623
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-837-732-4
 Query Match 76.4%; Score 68; DB 1; Length 19;
 Best Local Similarity 71.4%; Pred. No. 0.00039; Matches 10; Conservative 10; Length: 19; Pred. No. 0.00039; Mismatches 2; Indels 0; Gaps 0;
 Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 1 LNSWGCKGRICYT 14
 | ||||:|||
 6 LGIWCCKKLICYT 19
 RESULT 5
 US-08-472-597A-3
 Sequence 3, Application US/08472597A
 PATENT NO. 5624797
 GENERAL INFORMATION:
 APPLICANT: Bridon, D.P.
 APPLICANT: Sze, I.S.Y.
 APPLICANT: Dagħfal, D.J.
 APPLICANT: Jaffe, K.D.
 APPLICANT: Colpitts, T.L.
 TITLE OF INVENTION: Peptides for HIV-1 Detection
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ABBOTT LABORATORIES
 STREET: ONE HUNDRED ABBOTT PARK ROAD
 CITY: ABBOTT PARK
 STATE: IL
 COUNTRY: USA
 ZIP: 60064-3500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/472,597A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: POREMSKI, PRISCILLA E.
 REGISTRATION NUMBER: 33,207
 REFERENCE/DOCKET NUMBER: 5765.US.01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 708-937-6365
 TELEFAX: 708-938-2623
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-472-597A-3
 Query Match 76.4%; Score 68; DB 1; Length 19;
 Best Local Similarity 71.4%; Pred. No. 0.00039; Matches 10; Conservative 10; Length: 19; Pred. No. 0.00039; Mismatches 2; Indels 0; Gaps 0;
 Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 1 LNSWGCKGRICYT 14
 | ||||:|||
 6 LGIWCCKKLICYT 19

RESULT 6
US-08-837-732-3
Sequence 3, Application US/08837732
Patent No. 5800983
GENERAL INFORMATION:
APPLICANT: Bridon, D.P.
APPLICANT: Sze, I.S.Y.
APPLICANT: Daghfal, D.J.
APPLICANT: Jaffee, K.D.
APPLICANT: Copitts, T.L.
TITLE OF INVENTION: Peptides for HIV-1 Detection
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES
STREET: ONE HUNDRED ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
ZIP: 60064-3500
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/837,732
FILING DATE: 22-APR-1997
REFERENCE/DOCKET NUMBER: 5765.US.01
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/472,597
TELEPHONE: 708-937-5365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-837-732-3

RESULT 7
US-08-472-597A-2
Sequence 2, Application US/08472597A
Patent No. 5824979
GENERAL INFORMATION:
APPLICANT: Bridon, D.P.
APPLICANT: Sze, I.S.Y.
APPLICANT: Daghfal, D.J.
APPLICANT: Jaffee, K.D.
APPLICANT: Copitts, T.L.
TITLE OF INVENTION: Peptides for HIV-1 Detection
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES
STREET: ONE HUNDRED ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL

Query Match **70** **8%** **Score** **63**; **DB** **1**; **Le**
Best Local Similarity **64.3%**; **Pred.** **NO.** **0.0022**; **Le**
Matches **9**; **Conservative** **2**; **Mismatches** **3**

QY **1** **LNSWGCKGRICRYT** **14**
Db **6** **LGIWGCGSGKLCYT** **19**

COMPILED: 6/10/2001
 ZIP: 60644-3500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/472,597A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: POREMSKI, PRISCILLA E.
 REGISTRATION NUMBER: 33,207
 REFERENCE/DOCKET NUMBER: 5765.US.01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 708-937-6365
 TELEFAX: 708-938-2623
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-472-597A-2

RESULT 8
 US-08-837-732-2
 Sequence 2, Application US/08837732
 ; Sequence 2, Application US/08837732
 ; Patent No. 5800983
 ;
 GENERAL INFORMATION:
 Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0
 QY 1 LNSWIGKGRIGCT 14
 Db 6 LGIWGCKGKLICT 19

Query Match 66.3%; Score 59; DB 1; Length:19;
 Best Local Similarity 64.3%; Fred. No. 00088; 3; Indels 0; Gaps 0
 Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0

APPLICANT: Britton, D.P.
 APPLICANT: Size, I.S.Y.
 APPLICANT: Daghfal, D.J.
 APPLICANT: Jaffie, K.D.
 APPLICANT: Colbitts, T.L.
 TITLE OF INVENTION: Peptides for HTV-1 Detection
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ABBOTT LABORATORIES
 STREET: ONE HUNDRED ABBOTT PARK ROAD
 CITY: ABBOTT PARK
 STATE: IL
 COUNTRY: USA
 ZIP: 60064-3500

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/837-732
 FILING DATE: 22-APR-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/472,597
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: POREMSKI, PRISCILLA E.
 REGISTRATION NUMBER: 33,207
 REFERENCE/DOCKET NUMBER: 5765.US.01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 708-937-6365

TELEFAX: 708-938-2623

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 19 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-837-732-2

Query Match

Best Local Similarity 66.3%; Score 59; DB 1; Length 19;

Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LNSNGCKGRICYT 14

Db 6 LGTWGCKGKLICYT 19

RESULT 9

US-08-682-791B-7

Sequence 7, Application US/08682791B

PATENT NO. 6210901

GENERAL INFORMATION:

APPLICANT: SEIDEL, Christoph;

APPLICANT: HOESS, Eva;

APPLICANT: BAITZ Han-Georg

TITLE OF INVENTION: SPECIFIC BINDING SUBSTANCES FOR ANTIBODIES

NUMBER OF SEQUENCES: 33

TITLE OF INVENTION: AND THEIR USE FOR IMMUNOASSAYS OR VACCINES

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felte & Lynch

STREET: 805 Third Avenue

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10022

COMPUTER READABLE FORM:

MEDIAN TYPE: 3.5 inch 1.44 Mb storage diskette

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/682,791B

FILING DATE: July 31, 1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: NO. 6210901man D. Hanson

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: HUBR 1092

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 14

TYPE: amino acids

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE: OTHER INFORMATION: Xaa 1s homo-Phenylalanine

US-08-682-791B-8

Query Match

Best Local Similarity 62.9%; Score 56; DB 4; Length 14;

Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NSWGCKGRICYTS 15

Db 1 NSWGCAQRQVCHT 14

RESULT 11

US-08-682-791B-11

Sequence 11, Application US/08682791B

PATENT NO. 6210901

GENERAL INFORMATION:

APPLICANT: SEIDEL, Christoph;

APPLICANT: HOESS, Eva;

APPLICANT: BAITZ Han-Georg

TITLE OF INVENTION: SPECIFIC BINDING SUBSTANCES FOR ANTIBODIES

NUMBER OF SEQUENCES: 33

TITLE OF INVENTION: AND THEIR USE FOR IMMUNOASSAYS OR VACCINES

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felte & Lynch

STREET: 805 Third Avenue

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10022

us-09-603-3 / 3a-09_copy_12_2011

MOLECULE TYPE: peptide
US-08-765-452-7

RESULT 14
US-08-615-279-32
; sequence 32, Application US/08615279
; Patent No. 5804371
; GENERAL INFORMATION:
; APPLICANT: H SS, Eva
; APPLICANT: SEIDEL, Christoph
; APPLICANT: WIEHUES, Ursula-Henrike
; APPLICANT: FAMVZ, Elke
; APPLICANT: SCHMITT, Urban
; TITLE OF INVENTION: HAPPEN-LABELLED PEPTIDES
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP
; STREET: 655 Fifteenth Street, N. W., Suite 330 - G
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, version #1.30

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/615,279

; FILING DATE: 23-MAR-1995
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/02921
; FILING DATE: 24-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BERMAN, Richard J.
; REGISTRATION NUMBER: 39,107
; REFERENCE/DOCKET NUMBER: P564-6006

TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-5000
; TELEFAX: (202) 638-8810
; INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-765-452-11

Query Match 61.8%; Score 55; DB 2; Length 16;
; Best Local Similarity 53.3%; Pred. No. 0.03;
; Matches 8; Conservative 3; Mismatches 4;
; Indels 0; Gaps 0;

RESULT 15
US-08-765-452-11
; Sequence 11, Application US/08765452
; Patent No. 5981986
; GENERAL INFORMATION:
; APPLICANT: HERRMANN, Rupert
; APPLICANT: JOSEL, Hans-Peter
; APPLICANT: PAPPERT, Gunter
; APPLICANT: VOGTLE, Fritz
; APPLICANT: FROMBERGER, Bruno
; APPLICANT: ISSBERNER, Jorg
; TITLE OF INVENTION: HYDROPHILIC METAL COMPLEXES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAIDO, Marmelstein, Murray & Oram LLP
; STREET: 655 15th Street, N.W., Suite 330 - G St.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, version #1.30

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,452
; FILING DATE: 16-JAN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: JAHNS, Kristina M.
; REGISTRATION NUMBER: 41,092
; REFERENCE/DOCKET NUMBER: 564-6014

TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-5000
; TELEFAX: (202) 638-8810
; INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-765-452-11

Query Match 60.7%; Score 54; DB 1; Length 14;
; Best Local Similarity 57.1%; Pred. No. 0.037;
; Matches 8; Conservative 3; Mismatches 3;
; Indels 0; Gaps 0;

RESULT 16
US-07-033-964-8
; Sequence 8, Application US/07633964
; Patent No. 5459060
; GENERAL INFORMATION:
; APPLICANT: Cotropia MD, Joseph P
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES DIRECTED
; TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS (HIV-1)
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles S. Cotropia, Esq.
; STREET: 1201 Elm Street, Suite 4500
; CITY: Dallas
; STATE: TX
; COUNTRY: USA

Query Match 60.7%; Score 54; DB 1; Length 14;
; Best Local Similarity 57.1%; Pred. No. 0.037;
; Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
; OTHER INFORMATION: /note/
; OTHER INFORMATION: "digoxygenin-3-cme-epsilon-aminocaproic acid is attached to the 1 position."
; OTHER INFORMATION: Asn at the 1 position."
; US-08-615-279-32

Query Match 15
; Sequence 15, Application US/08615279
; Patent No. 5804371
; GENERAL INFORMATION:
; APPLICANT: NIKAIDO, Marmelstein, Murray & Oram LLP
; TITLE OF INVENTION: HAPPEN-LABELLED PEPTIDES
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAIDO, Marmelstein, Murray & Oram LLP
; STREET: 655 Fifteenth Street, N. W., Suite 330 - G
; CITY: Washington
; STATE: DC
; COUNTRY: USA

Query Match 14
; Sequence 14, Application US/08765452
; Patent No. 5981986
; GENERAL INFORMATION:
; APPLICANT: PAPPERT, Gunter
; APPLICANT: VOGTLE, Fritz
; APPLICANT: FROMBERGER, Bruno
; APPLICANT: ISSBERNER, Jorg
; TITLE OF INVENTION: HYDROPHILIC METAL COMPLEXES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAIDO, Marmelstein, Murray & Oram LLP
; STREET: 655 15th Street, N.W., Suite 330 - G St.
; CITY: Washington
; STATE: DC
; COUNTRY: USA

Query Match 15
; Sequence 15, Application US/07633964
; Patent No. 5459060
; GENERAL INFORMATION:
; APPLICANT: Cotropia MD, Joseph P
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES DIRECTED
; TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS (HIV-1)
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles S. Cotropia, Esq.
; STREET: 1201 Elm Street, Suite 4500
; CITY: Dallas
; STATE: TX
; COUNTRY: USA

COUNTRY: USA
 ZIP: 60064-3500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/472,597A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: POREMSKI, PRISCILLA E.
 REGISTRATION NUMBER: 33,207
 REFERENCE/DOCKET NUMBER: 5765.US.01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 708-937-6365
 TELEX: 708-938-2623
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-472-597A-1

RESULT 20

Query Match 60.7%; Score 54; DB 1; Length 19;
 Best Local Similarity 57.1%; Pred. No. 0.049; 4; Indels
 Matches 8; Conservative 2; Mismatches 4; Gaps 0;
 Qy 1 LNSWGKGRICYT 14
 | ||| :||| |
 Db 6 LGIWGCGSGKLCIT 19

US-08-837-732-1

Query Match 60.7%; Score 54; DB 1; Length 19;
 Best Local Similarity 57.1%; Pred. No. 0.049; 4; Indels
 Matches 8; Conservative 2; Mismatches 4; Gaps 0;
 Qy 1 LNSWGKGRICYT 14
 | ||| :||| |
 Db 6 LGIWGCGSGKLCIT 19

RESULT 21

Query Match 60.7%; Score 54; DB 1; Length 19;
 Best Local Similarity 57.1%; Pred. No. 0.049; 4; Indels
 Matches 8; Conservative 2; Mismatches 4; Gaps 0;
 Qy 1 LNSWGKGRICYT 14
 | ||| :||| |
 Db 6 LGIWGCGSGKLCIT 19

US-08-146-028-5

Sequence 5, Application US/08146028
 Patent No. 5891640
 GENERAL INFORMATION:
 APPLICANT:
 APPLICANT: Bridon, D.P.
 APPLICANT: Sze, I.S.Y.
 APPLICANT: Baghfi, D.J.
 APPLICANT: Jaffe, K.D.
 APPLICANT: Colpits, T.L.
 TITLE OF INVENTION: Peptides for HIV-1 Detection
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ABBOTT LABORATORIES
 STREET: ONE HUNDRED ABBOTT PARK ROAD
 CITY: ABBOTT PARK
 STATE: IL
 COUNTRY: USA
 ZIP: 60064-3500
 COMPUTER READABLE FORM:
 COMPUTER TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/146,028
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 12 amino acids
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: Ant70
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 1
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 12
 US-08-146-028-5

RESULT 22

Query Match 59.6%; Score 53; DB 2; Length 12;
 Best Local Similarity 66.7%; Pred. No. 0.045; 3; Indels
 Matches 6; Conservative 3; Mismatches 0; Gaps 0;
 Qy 4 WGCKGRIC 12
 | ||| :||| |
 Db 3 WGCKGKLV 11

US-08-23-425A-5

Sequence 5, Application US/08723425A
 Patent No. 6165730
 GENERAL INFORMATION:
 APPLICANT: DELEUR, ROBERT
 TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF
 TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT
 TITLE OF INVENTION: EPITOPE AND THEIR USE IN A PROCESS FOR DETERMINATION OF

us-09-605-5/3a-69_copy_12_28.1am

TITLE OF INVENTION: ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING . . .

NUMBER OF SEQUENCES: 453

CORRESPONDENCE ADDRESS:

ADDRESSE: NIXON & VANDERHVE, P.C.

STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR

CITY: Arlington

STATE: VA

COUNTRY: USA

ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/723,425A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: SADOFF, B.J.

REGISTRATION NUMBER: 36,663

REFERENCE/DOCKET NUMBER: 1487-13

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-816-4100

TELEFAX: 703-816-4100

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

MOLECULE TYPE: peptide

LENGTH: 12 amino acids

TOPOLOGY: linear

TYPE: amino acid

TOPOLOGY: linear

HYPOTHETICAL: NO

INDIVIDUAL ISOLATE: Ant70

FEATURE:

NAME/KEY: Modified-site

LOCATION: 1

NAME/KEY: Modified-site

LOCATION: 12

NAME/KEY: Modified-site

LOCATION: 1

NAME/KEY: Modified-site

LOCATION: 12

RESULT 24

US-09-009-953-131

Sequence 131, Application US/09009953

; Patent No. 6413517

GENERAL INFORMATION:

APPLICANT: Sette, Alessandro

TITLE OF INVENTION: Identification of Broadly Reactive DR Restricted Epitopes

NUMBER OF SEQUENCES: 274

CORRESPONDENCE ADDRESS:

ADDRESSE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/009,953

FILING DATE: 21-Jan-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/036,713

FILING DATE: 23-JAN-1997

APPLICATION NUMBER: US 60/037,432

FILING DATE: 07-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: Weber, Eileen Lauver

REGISTRATION NUMBER: 32,762

REFERENCE/DOCKET NUMBER: 018623-011520US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-576-0200

TELEX: 415-576-0300

INFORMATION FOR SEQ ID NO: 131:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 131:

ATTORNEY/AGENT INFORMATION:

NAME: Weber, Eileen Lauver

REGISTRATION NUMBER: 32,762

REFERENCE/DOCKET NUMBER: 018623-011520US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-576-0200

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 131:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 131:

US-09-009-953-131

RESULT 25

US-07-901-874B-14

Query Match 59.6%; Score 53; DB 1; Length 16;

Best Local Similarity 58.3%; Pred. No. 0.059;

Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 4 WGCKGRICYS 15

Db 1 WGCSGKLICTTA 12

RESULT 26

US-07-901-865-14

Query Match 59.6%; Score 53; DB 1; Length 16;

Best Local Similarity 58.3%; Pred. No. 0.059;

Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 4 WGCKGRICYS 15

Db 1 WGCKGRICYS 15

RESULT 27

US-07-633-964-14

Query Match 59.6%; Score 53; DB 1; Length 19;

Best Local Similarity 58.3%; Pred. No. 0.077;

Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 4 WGCKGRICYS 15

Db 2 WGCSGKLICTTA 13

RESULT 25

US-07-901-874B-14

Sequence 14, Application US/07901874B.

Patent No. 5476765

GENERAL INFORMATION:

APPLICANT: Chang Yi Wang

TITLE OF INVENTION: SYNTHETIC PEPTIDE COMPOSITIONS WITH IMMUNOREACTIVITIES TO ANTIBODIES TO HTLV AND AS

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/901, 874B

FILING DATE: 22-JUN-1992

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/469, 291

FILING DATE: 13-JAN-1989

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/469, 291

FILING DATE: 13-JAN-1989

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/297, 635

FILING DATE: 13-JAN-1989

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/297, 635

FILING DATE: 13-JAN-1989

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/001, 885

FILING DATE: 9-JAN-1987

ATTORNEY/AGENT INFORMATION:

NAME: MARTA C.H. LIN

REGISTRATION NUMBER: 29,323

REFERENCE/DOCKET NUMBER: 1151-4026 US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800

TELEFAX: (212) 751-6849

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 19

TYPE: Amino acid

STRANDEDNESS: Single

TOPOLOGY: Unknown

MOLECULE TYPE: Peptide

US-07-901-874B-14

RESULT 26

US-07-901-865-14

Sequence 14, Application US/08457865

Patent No. 5681696

GENERAL INFORMATION:

APPLICANT: Chang Yi Wang

TITLE OF INVENTION: SYNTHETIC PEPTIDE COMPOSITIONS WITH IMMUNOREACTIVITIES TO ANTIBODIES TO HTLV AND AS

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/457, 865

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/901, 874

FILING DATE: 22-JUN-1992

APPLICATION NUMBER: US 07/469, 291

FILING DATE: 24-JAN-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/297, 635

FILING DATE: 13-JAN-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/001, 885

FILING DATE: 9-JAN-1987

ATTORNEY/AGENT INFORMATION:

NAME: MARTA C.H. LIN

REGISTRATION NUMBER: 29,323

REFERENCE/DOCKET NUMBER: 1151-4026 US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800

TELEFAX: (212) 751-6849

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 19

TYPE: Amino acid

STRANDEDNESS: Single

TOPOLOGY: Unknown

MOLECULE TYPE: Peptide

US-08-477-865-14

RESULT 27

US-07-633-964-14

Query Match 59.6%; Score 53; DB 1; Length 19;

Best Local Similarity 58.3%; Pred. No. 0.077;

Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 4 WGCKGRICYS 15

Db 2 WGCSGKLICTTA 13

RESULT 27

US-07-633-964-14

Sequence 14, Application US/07633964

Patent No. 545960

GENERAL INFORMATION:

APPLICANT: Cotorria MD, Joseph P

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES DIRECTED

TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS (HIV-1)

NUMBER OF SEQUENCES: 42

NUMBER OF SEQUENCES: 453
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patientin Release #1.0, version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,028
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: HIV-1
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
FEATURE:
NAME/KEY: Modified-site
LOCATION: 21
US-08-146-028-2

Query Match 59.6% Score 53; DB 2; Length 21;
Best Local Similarity 58.3%; Pred. No. 0.076;
Matches 7; Conservative 3; Mismatches 2; Indels 0;
Gaps 0;
QY 4 WCKGRICRYS 15
Db 3 WCGSGKLLCTTA 14

Search completed: June 5, 2003, 07:23:12
Job time : 15 secs

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 5, 2003, 07:21:57 ; Search time 228 Seconds
(without alignments)

6.792 Million cell updates/sec

Title: US-09-605-573A-69_COPY_12_26

Perfect score: 89

Sequence: 1 LNSWQCKGRICRYS 15

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 392085 seqs, 103240269 residues

Total number of hits satisfying chosen parameters: 80475

Minimum DB seq length: 0

Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

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14: /cgn2_6/ptodata/1/pubpa/US60_PUBCOMB_pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	51	57.3	21 9	US-09-845-042-23
5	50	56.2	16 9	US-09-423-863-3
6	49	55.1	10 10	US-09-839-666-10
7	49	55.1	16 9	US-09-433-863-1
8	42	47.2	17 9	US-09-388-847-1
9	40	44.9	9 1	US-09-821-739A-78
10	40	44.9	9 10	US-09-894-018-80
11	40	44.9	9 10	US-09-894-018-185
12	40	44.9	10 10	US-09-765-086-43
13	37	41.6	16 9	US-10-741-41
14	36	40.4	10 1	US-08-821-739A-90
15	36	40.4	20 9	US-09-910-009A-481
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51	27	30.3	12 10	US-09-784-887B-5
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67	26	29.2	8 9	US-10-094-401-182
68	26	29.2	9 9	US-09-835-948-38
69	26	29.2	9 10	US-09-930-174-42
70	26	29.2	10 9	US-09-572-04B-2113
71	26	29.2	10 9	US-09-577-404B-2155
72	26	29.2	11 10	US-09-078-070-26
73	26	29.2	12 9	US-10-0-0-9-261-297
74	26	29.2	12 9	US-10-0-0-9-261-297
75	26	29.2	14 10	US-10-0-0-4-01-230
76	26	29.2	14 10	US-09-477-079A-18
77	26	29.2	15 9	US-10-0-0-0-0-9-14
78	26	29.2	15 9	US-09-987-961-18
79	26	29.2	15 9	US-09-987-961-18
80	26	29.2	15 9	US-09-987-961-18
81	26	29.2	15 9	US-09-987-961-20
82	26	29.2	15 9	US-09-987-961-25
83	26	29.2	15 9	US-09-987-961-27
84	26	29.2	16 9	US-09-910-009A-408
85	26	29.2	17 9	US-09-846-001-8
86	26	29.2	17 9	US-10-12-256-16
87	26	29.2	18 10	US-09-864-761-38674
88	26	29.2	18 10	US-09-77-029A-17
89	26	29.2	19 10	US-09-864-761-37007
90	26	29.2	20 8	US-08-922-711-8
91	26	29.2	20 9	US-09-843-676-194
92	26	29.2	20 9	US-09-973-025-75
93	26	29.2	20 9	US-09-973-025-75
94	26	29.2	20 9	US-09-973-025-75
95	26	29.2	20 9	US-09-973-025-75
96	26	29.2	20 9	US-09-973-025-75
97	26	29.2	20 9	US-09-973-025-75
98	26	29.2	20 9	US-09-973-025-75
99	26	29.2	20 9	US-09-973-025-75
100	26	29.2	20 9	US-09-973-025-75
101	26	29.2	20 9	US-09-973-025-75
102	26	29.2	20 9	US-09-973-025-75
103	26	29.2	20 9	US-09-973-025-75
104	26	29.2	20 9	US-09-973-025-75
105	26	29.2	20 9	US-09-973-025-75
106	26	29.2	20 9	US-09-973-025-75
107	26	29.2	20 9	US-09-973-025-75
108	26	29.2	20 9	US-09-973-025-75
109	26	29.2	20 9	US-09-973-025-75
110	26	29.2	20 9	US-09-973-025-75
111	26	29.2	20 9	US-09-973-025-75
112	26	29.2	20 9	US-09-973-025-75
113	26	29.2	20 9	US-09-973-025-75
114	26	29.2	20 9	US-09-973-025-75
115	26	29.2	20 9	US-09-973-025-75
116	26	29.2	20 9	US-09-973-025-75
117	26	29.2	20 9	US-09-973-025-75
118	26	29.2	20 9	US-09-973-025-75
119	26	29.2	20 9	US-09-973-025-75
120	26	29.2	20 9	US-09-973-025-75
121	26	29.2	20 9	US-09-973-025-75
122	26	29.2	20 9	US-09-973-025-75
123	26	29.2	20 9	US-09-973-025-75
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125	26	29.2	20 9	US-09-973-025-75
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128	26	29.2	20 9	US-09-973-025-75
129	26	29.2	20 9	US-09-973-025-75
130	26	29.2	20 9	US-09-973-025-75
131	26	29.2	20 9	US-09-973-025-75
132	26	29.2	20 9	US-09-973-025-75
133	26	29.2	20 9	US-09-973-025-75
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138	26	29.2	20 9	US-09-973-025-75
139	26	29.2	20 9	US-09-973-025-75
140	26	29.2	20 9	US-09-973-025-75
141	26	29.2	20 9	US-09-973-025-75
142	26	29.2	20 9	US-09-973-025-75
143	26	29.2	20 9	US-09-973-025-75
144	26	29.2	20 9	US-09-973-025-75
145	26	29.2	20 9	US-09-973-025-75
146	26	29.2	20 9	US-09-973-025-75
147	26	29.2	20 9	US-09-973-025-75
148	26	29.2	20 9	US-09-973-025-75
149	26	29.2	20 9	US-09-973-025-75
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155	26	29.2	20 9	US-09-973-025-75
156	26	29.2	20 9	US-09-973-025-75
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158	26	29.2	20 9	US-09-973-025-75
159	26	29.2	20 9	US-09-973-025-75
160	26	29.2	20 9	US-09-973-025-75
161	26	29.2	20 9	US-09-973-025-75
162	26	29.2	20 9	US-09-973-025-75
163	26	29.2	20 9	US-09-973-025-75
164	26	29.2	20 9	US-09-973-025-75
165	26	29.2	20 9	US-09-973-025-75
166	26	29.2	20 9	US-09-973-025-75
167	26	29.2	20 9	US-09-973-025-75
168	26	29.2	20 9	US-09-973-025-75
169	26	29.2	20 9	US-09-973-025-75
170	26	29.2	20 9	US-09-973-025-75
171	26	29.2	20 9	US-09-973-025-75
172	26	29.2	20 9	US-09-973-025-75
173	26	29.2	20 9	US-09-973-025-75
174	26	29.2	20 9	US-09-973-025-75
175	26	29.2	20 9	US-09-973-025-75
176	26	29.2	20 9	US-09-973-025-75
177	26	29.2	20 9	US-09-973-025-75
178	26	29.2	20 9	US-09-973-025-75
179	26	29.2	20 9	US-09-973-025-75
180	26			

us-09-605-573a-69_copy_12_26.Fa.pn

Qy 1 LNSWGCKGRIC 12
Db 10 LGIWCSCKLIC 21

RESULT 5
US-09-423-863-3
; Sequence 3, Application US/09423863
; Publication No. US20030054336A1
; GENERAL INFORMATION:
; APPLICANT: Donie, Frederic
; APPLICANT: Faatz, Elke

; APPLICANT: Hoess, Eva
; TITLE OF INVENTION: PROCESS FOR THE DETECTION OF HIV ANTIBODIES AND
; TITLE OF INVENTION: ANTIGENS USED IN IT
; FILE REFERENCE: BMD 9974 4638/OP/US-SZ
; CURRENT APPLICATION NUMBER: US/09/423, 863
; CURRENT FILING DATE: 2000-02-08
; EARLIER APPLICATION NUMBER: DE 19720914.9
; EARLIER FILING DATE: 1997-05-16
; EARLIER APPLICATION NUMBER: PCT/EP98/02816
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 3
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-423-863-3

Query Match 56.2%; Score 50; DB 9; Length 16;
Best Local Similarity 53.3%; Pred. No. 0.23;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LNSWGCKGRIC 15
Db 1 LGIWCSCKLIC 15

RESULT 6
US-09-423-863-6
; Sequence 6, Application US/09423863
; Publication No. US20030054336A1
; GENERAL INFORMATION:
; APPLICANT: Donie, Frederic
; APPLICANT: Faatz, Elke

; APPLICANT: Hoess, Eva
; TITLE OF INVENTION: PROCESS FOR THE DETECTION OF HIV ANTIBODIES AND
; TITLE OF INVENTION: ANTIGENS USED IN IT
; FILE REFERENCE: BMD 9974 4638/OP/US-SZ
; CURRENT APPLICATION NUMBER: US/09/423, 863
; CURRENT FILING DATE: 2000-02-08
; EARLIER APPLICATION NUMBER: DE 19720914.9
; EARLIER FILING DATE: 1997-05-16
; EARLIER APPLICATION NUMBER: PCT/EP98/02816
; EARLIER FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 6
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-423-863-6

Query Match 56.2%; Score 50; DB 9; Length 16;
Best Local Similarity 53.3%; Pred. No. 0.23;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LNSWGCKGRIC 15
Db 1 LGIWCSCKLIC 15

RESULT 7
US-09-839-666-10
; Sequence 10, Application US/09839666
; Publication No. US20030025513A1
; GENERAL INFORMATION:
; APPLICANT: SALIBERG, MATTI
; TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DARBY & DARBY PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/839, 666
; FILING DATE: 19 Apr-2001
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08-737, 085
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Rea
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 3846/0C569
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7659
; TELEFAX: 212-753-6237
; TELEX: 236687

; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-839-666-10

Query Match 55.1%; Score 49; DB 10; Length 10;
Best Local Similarity 66.7%; Pred. No. 0.21;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 WACKGRIC 12
Db 1 WCGSKLIC 9

RESULT 8
US-09-423-863-1
; Sequence 1, Application US/09423863
; Publication No. US20030054336A1
; GENERAL INFORMATION:
; APPLICANT: Donie, Frederic
; APPLICANT: Faatz, Elke
; APPLICANT: Hoess, Eva
; TITLE OF INVENTION: PROCESS FOR THE DETECTION OF HIV ANTIBODIES AND
; TITLE OF INVENTION: ANTIGENS USED IN IT
; FILE REFERENCE: BMD 9974 4638/OP/US-SZ
; CURRENT APPLICATION NUMBER: US/09/423, 863
; CURRENT FILING DATE: 2000-02-08
; EARLIER APPLICATION NUMBER: DE 19720914.9
; EARLIER FILING DATE: 1997-05-16
; EARLIER APPLICATION NUMBER: PCT/EP98/02816
; EARLIER FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn ver. 2.1
 SEQ ID NO 1
 LENGTH: 16
 TYPE: PRT
 ORGANISM: Human immunodeficiency virus type 1
 US-09-423-863-1

Query Match 55.1%; Score 49; DB 9; Length 16;
 Best Local Similarity 57.1%; Pred. No. 0.32;
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 Oy 1 LNSWGCGRCIGCT 14
 Db 1 LGIWGCGSHKICCT 14

RESULT 9
 US-09-388-847-1
 Sequence 1, Application US/09388847
 Publication No. US20030004320A1
 GENERAL INFORMATION:
 APPLICANT: Annunziato, Michael E
 Palumbo, Paul S
 TITLE OF INVENTION: Activated Peptides and Conjugates
 NUMBER OF SEQIDNOS: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hoechst Celanese Corporation
 STREET: Route 202-206, P. O. Box 2500
 CITY: Somerville
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 08876-1258

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK (IBM PC COMPATIBLE)
 COMPUTER: DELL 4100/MXV (IBM PC COMPATIBLE)
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WordPerfect for Windows, Version #6.0a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/388,847
 FILING DATE: 02-SEP-1999
 CLASSIFICATION: <Unknown>
 PRIORITY DATA:
 APPLICATION NUMBER: US/08/033,546
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Rosenstock, Jerome
 REGISTRATION NUMBER: 25,456
 REFERENCE/DOCKET NUMBER: BD11005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 221-2125
 TELEFAX: (908) 231-4919
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 17 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-09-388-847-1

Query Match 44.9%; Score 40; DB 1; Length 9;
 Best Local Similarity 62.5%; Pred. No. 3.5e+01; Mismatches 2; Indels 0; Gaps 0;
 Oy 4 WACKGRIL 11
 Db 2 WGCGKLL 9

RESULT 11
 US-09-894-018-80
 Sequence 80, Application US/09894018
 Patent No. US2002119127A1
 GENERAL INFORMATION:
 APPLICANT: EPIIMMUNE, INC.
 APPLICANT: Sette, Alessandro
 APPLICANT: Chestnut, Robert
 APPLICANT: Livingston, Brian
 APPLICANT: Baker, Denis W
 APPLICANT: Newman, Mark
 APPLICANT: Brown, David
 TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
 TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY
 FILE REFERENCE: 39963-20033.00
 CURRENT APPLICATION NUMBER: US/09/894,018
 CURRENT FILING DATE: 2001-06-27
 PRIORITY NUMBER: PCT/US00/35568
 PRIORITY FILING DATE: 2000-12-28
 PRIORITY NUMBER: US 60/173,390
 PRIORITY FILING DATE: 1999-12-28
 PRIORITY NUMBER: US 60/284,221
 PRIORITY FILING DATE: 2001-04-16
 NUMBER OF SEQ ID NOS: 368
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 80
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Artificial Sequence

RESULT 10
 US-08-821-739A-78
 Sequence 78, Application US/08821739A
 Patent No. US20020168374A1

; FEATURE:
 ; OTHER INFORMATION: Oligopeptide
 US-09-894-018-80

; Query Match
 Best Local Similarity 44.9%; Score 40; DB 10; Length 9;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 4 WGCKGRIL 11
 Db 2 WGCSGKLI 9

RESULT 12
 US-09-894-018-185
 ; Sequence 185, Application US/09894018
 ; Patent No. US2002019127A1
 ; GENERAL INFORMATION:
 ; APPLICANT: EPIMMUNE, Inc.
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Chestnut, Robert
 ; APPLICANT: Livingston, Brian
 ; APPLICANT: Baker, Denis
 ; APPLICANT: Newman, Mark
 ; APPLICANT: Brown, David
 ; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
 ; TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY
 ; FILE REFERENCE: 39563-20033.00
 ; CURRENT APPLICATION NUMBER: US/09/894, 018
 ; CURRENT FILING DATE: 2001-06-27
 ; PRIOR APPLICATION NUMBER: PCT/US00/355568
 ; PRIOR FILING DATE: 2000-12-28
 ; PRIOR APPLICATION NUMBER: US 60/173, 390
 ; PRIOR FILING DATE: 1999-12-28
 ; PRIOR APPLICATION NUMBER: US 60/284, 221
 ; PRIOR FILING DATE: 2001-04-16
 ; NUMBER OF SEQ ID NOS: 368
 ; SOFTWARE: FASTSEQ for Windows version 4.0
 ; SEQ ID NO 185
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Transgenic mouse
 ; LENGTH: 185

US-09-894-018-185

Query Match
 Best Local Similarity 44.9%; Score 40; DB 10; Length 9;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 4 WGCKGRIL 11
 Db 2 WGCSGKLI 9

RESULT 13
 US-09-765-086-43
 ; Sequence 43, Application US/09765086
 ; Patent No. US2001046498A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruoslahti, Erkki
 ; APPLICANT: Pasqualini, Renata
 ; APPLICANT: Radh, Arap
 ; APPLICANT: Bredesen, Dale E.
 ; APPLICANT: Ellerby, H. Michael
 ; TITLE OF INVENTION: Chimeric Prostate-Homing Peptides With
 ; FILE REFERENCE: P-LW 3844
 ; CURRENT APPLICATION NUMBER: US/09/765, 086
 ; CURRENT FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: US 09/489, 582
 ; PRIOR FILING DATE: 2000-01-21
 ; NUMBER OF SEQ ID NOS: 235
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 43

; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: synthetic peptide
 US-09-765-086-43

Query Match
 Best Local Similarity 41.6%; Score 37; DB 10; Length 10;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 WGCKGR 9
 Db 2 WGCGNR 7

RESULT 14
 US-10-026-741-41
 ; Sequence 41, Application US/10026741
 ; Publication No. US20030049604A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHARNEAU, PIERRE
 ; APPLICANT: CLAVEL, FRANCOISE
 ; APPLICANT: BORMAN, ANDREW
 ; OUTLLET, CAROLINE
 ; GUETARD, DENISE
 ; MONTAIGNE, LUC
 ; DONJON DE SAINT-MARTIN, JACQUELINE
 ; COHEN, JAQUES
 ; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HTV-1 TYPE (OR
 ; NUMBER OF SEQUENCES: SUBTYPE) ANTIGENS
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Finegan, Henderson, Farabow, Garrett &
 ; Dunner, L. P.
 ; STREET: 1300 I Street, N.W.
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005-3315

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patientin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/026,741
 FILING DATE: 27-Dec-2001
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/817,441
 FILING DATE: 31-AUG-1998
 APPLICATION NUMBER: PCT/FR 95/01391
 FILING DATE: 20-OCT-1995
 APPLICATION NUMBER: FR 9412554
 FILING DATE: 20-OCT-1994
 APPLICATION NUMBER: FR 9502526
 FILING DATE: 03-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Meyers, Kenneth J.
 REGISTRATION NUMBER: 25,146
 REFERENCE/DOCKET NUMBER: 03260-6005-00000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-408-4000
 TELEFAX: 202-408-4400
 INFORMATION FOR SEQ ID NO: 41:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 41:
 US-10-026-741-41

Query Match 40.4%; Score 36; DB 9; Length 6;
 Best Local Similarity 83.3%; Pred. No. 3.5e+05; Mismatches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 WCKGR 9
 Db 1 WGCKNR 6

RESULT 15
 US-08-821-739A-90
 Sequence 90, Application US/08821739A
 Patent No. US20020168374A1

GENERAL INFORMATION:

APPLICANT: Kubo, Ralph T.
 APPLICANT: Grey, Howard M.
 APPLICANT: Sette, Alessandro
 APPLICANT: Celis, Esteban

TITLE OF INVENTION: HLA Binding Peptides and Their Uses

CURRENT APPLICATION NUMBER: US/08/821,739A
 CURRENT FILING DATE: 1999-03-20
 PRIOR APPLICATION NUMBER: 60/013,833
 PRIOR FILING DATE: 1996-03-21
 PRIOR APPLICATION NUMBER: 08/589,107
 PRIOR FILING DATE: 1996-07-12
 PRIOR APPLICATION NUMBER: 08/451,913
 PRIOR FILING DATE: 1995-05-26
 PRIOR APPLICATION NUMBER: 08/347,610
 PRIOR FILING DATE: 1994-12-01
 PRIOR APPLICATION NUMBER: 08/186,266
 PRIOR FILING DATE: 1994-01-25
 PRIOR APPLICATION NUMBER: 08/159,339
 PRIOR FILING DATE: 1993-11-29
 PRIOR APPLICATION NUMBER: 08/103,396
 PRIOR FILING DATE: 1993-08-06
 PRIOR APPLICATION NUMBER: 08/027,746
 PRIOR FILING DATE: 1993-03-05
 PRIOR APPLICATION NUMBER: 07/926,666
 PRIOR FILING DATE: 1992-08-07
 NUMBER OF SEQ ID NOS: 149
 SOFTWARE: PatentIn version 3.1.
 SEQ ID NO 90
 LENGTH: 10
 TYPE: PRP
 ORGANISM: Homo sapiens

US-08-821-739A-90

Query Match 40.4%; Score 36; DB 1; Length 10;
 Best Local Similarity 55.6%; Pred. No. 21; Mismatches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LNSWGCKR 9
 Db 2 LGIWGCSK 10

RESULT 16
 US-09-910-0029A-481
 Sequence 481, Application US/09910009A
 Publication No. US20030052341

GENERAL INFORMATION:

APPLICANT: University of Utah Research Foundation
 APPLICANT: Cognex, Inc.
 APPLICANT: Olivera, Baldomero M.
 APPLICANT: McIntosh, J. Michael
 APPLICANT: Garrett, James E.
 APPLICANT: Watkins, Maren
 APPLICANT: Cruz, Lourdes J.
 APPLICANT: Shon, Ki-Joon
 APPLICANT: Jacobsen, Richard
 APPLICANT: Jones, Robert M.

Query Match 39.3%; Score 35; DB 9; Length 20;
 Best Local Similarity 33.3%; Pred. No. 57; Mismatches 5; Conservative 4; Mismatches 2; Indels 4; Gaps 1;

Qy 3 SWGC---KGRTCY 13
 Db 3 SWPCPRIISNGKLUVCF 17

RESULT 17
 US-10-026-741-5
 Sequence 5, Application US/10026741
 Publication No. US2003004960A1

GENERAL INFORMATION:

APPLICANT: CHARNEAU, PIERRE
 CLAVEL, FRANCOISE
 BORMAN, ANDREW
 OUILLENT, CAROLINE
 GUTIARD, DENISE
 MONTAGNER, LUC
 DONJON DE SAINT-MARTIN, JACQUELINE
 COHEN, JACQUES

TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR SUBTYPE) ANTIGENS

NUMBER OF SEQUENCES: 103

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Finnean, Henderson, Farabow, Garrett & Dunner, L.L.P.
 STREET: 1300 I Street, N.W.
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005-3315

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/026,741
 FILING DATE: 27-Dec-2001

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/817,441
 FILING DATE: 31-AUG-1998
 APPLICATION NUMBER: PCT/FR 95/01391
 FILING DATE: 20-OCT-1995
 APPLICATION NUMBER: FR 9412554
 FILING DATE: 20-OCT-1994
 APPLICATION NUMBER: FR 9502526
 FILING DATE: 03-MAR-1995

APPLICANT: Cartier, G. Edward
 APPLICANT: Shen, Greg S.
 APPLICANT: Wagstaff, John D.
 TITLE OF INVENTION: Mu-Conopeptides
 FILE REFERENCE: 2314-242

CURRENT APPLICATION NUMBER: US/09/910,009A
 CURRENT FILING DATE: 2001-07-23
 PRIOR APPLICATION NUMBER: US 60/219,619
 PRIOR FILING DATE: 2000-07-21

PRIOR APPLICATION NUMBER: US 60/245,157
 PRIOR FILING DATE: 2000-11-03

PRIOR APPLICATION NUMBER: US 60/264,319
 PRIOR FILING DATE: 2001-01-29

PRIOR APPLICATION NUMBER: US 60/277,270
 PRIOR FILING DATE: 2001-03-21

NUMBER OF SEQ ID NOS: 520
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 481
 LENGTH: 20
 TYPE: PRP
 ORGANISM: Canus ermineus

US-09-910-009A-481

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.

REGISTRATION NUMBER: 25-146

REFERENCE/DOCKET NUMBER: 03260.6005-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 7 amino acids

TYPE: amino acid

STRANDBNESS: Single

TOPOLOGY: linear

MOLECULE TYPE: Peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-10-026-741-5

Query Match 38.2%; Score 34; DB 9; Length 7;
 Best Local Similarity 71.4%; Pred. No. 3.5e-05; 5;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CKGRIC 12
 Db 1 CKNRIC 7

RESULT 18

US-09-423-863-10

Sequence 10, Application US/09423863

Publication No. US20030054336A1

GENERAL INFORMATION:

APPLICANT: Donie, Frederic

APPLICANT: Faatz, Elke

APPLICANT: Hoess, Eva

TITLE OF INVENTION: PROCESS FOR THE DETECTION OF HIV ANTIBODIES AND

TITLE OF INVENTION: ANTIGENS USED IN IT

FILE REFERENCE: BMD9 9974 4638/OP/US/SZ

CURRENT APPLICATION NUMBER: US/09/423, 863

CURRENT FILING DATE: 2000-02-08

EARLIER APPLICATION NUMBER: DE 19720914.9

EARLIER FILING DATE: 1997-05-16

EARLIER APPLICATION NUMBER: PCT/EP98/02816

EARLIER FILING DATE: 1998-05-13

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO: 10

LENGTH: 10

TYPE: PRT

ORGANISM: Human immunodeficiency virus type 1

US-09-423-863-10

Query Match 38.2%; Score 34; DB 9; Length 10;
 Best Local Similarity 60.0%; Pred. No. 44; 6;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CKGRIC 15
 Db 1 CSGRHICTT 10

RESULT 20

US-09-423-863-9

Sequence 9, Application US/09423863

Publication No. US20030054336A1

GENERAL INFORMATION:

APPLICANT: Donie, Frederic

APPLICANT: Faatz, Elke

APPLICANT: Hoess, Eva

TITLE OF INVENTION: PROCESS FOR THE DETECTION OF HIV ANTIBODIES AND

TITLE OF INVENTION: ANTIGENS USED IN IT

FILE REFERENCE: BMD9 9974 4638/OP/US/SZ

CURRENT APPLICATION NUMBER: US/09/423, 863

CURRENT FILING DATE: 2000-02-08

EARLIER APPLICATION NUMBER: DE 19720914.9

EARLIER FILING DATE: 1997-05-16

EARLIER APPLICATION NUMBER: PCT/EP98/02816

EARLIER FILING DATE: 1998-05-13

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO: 9

LENGTH: 10

TYPE: PRT

ORGANISM: Human immunodeficiency virus type 1

US-09-423-863-9

Query Match 38.2%; Score 33; DB 9; Length 10;
 Best Local Similarity 66.7%; Pred. No. 62; 6;
 Matches 6; Conservative 0; Mismatches 0; Indels 3; Gaps 0;

Qy 6 CKGRIC 14
 Db 1 CSGRHICTT 9

RESULT 21

US-09-845-612B-14

Sequence 14, Application US/09845612B

Publication No. US20030083261A1

GENERAL INFORMATION:

APPLICANT: YU, HONGTAO

APPLICANT: TANG, ZHANYUN

APPLICANT: LUO, XUELIAN

APPLICANT: RIZZO-BY, JOSE

TITLE OF INVENTION: A CLASS OF 12MER PEPTIDES THAT INHIBIT THE FUNCTION OF THE MIT

TITLE OF INVENTION: POINT PROTEIN MAD2

FILE REFERENCE: US20030083261A1

CURRENT APPLICATION NUMBER: US/09/845, 612B

CURRENT FILING DATE: 2001-04-27

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin version 3.0

SEQ ID NO: 14

LENGTH: 15

RESULT 19

US-09-423-863-11

Sequence 11, Application US/09423863

Publication No. US20030054336A1

GENERAL INFORMATION:

APPLICANT: Donie, Frederic

APPLICANT: Faatz, Elke

APPLICANT: Hoess, Eva

TITLE OF INVENTION: PROCESS FOR THE DETECTION OF HIV ANTIBODIES AND

TITLE OF INVENTION: ANTIGENS USED IN IT

FILE REFERENCE: BMD9 9974 4638/OP/US/SZ

CURRENT APPLICATION NUMBER: US/09/423, 863

CURRENT FILING DATE: 2000-02-08

TYPE: PRT
 ORGANISM: Drosophila
 US-09-845-612B-14

Query Match 37.1%; Score 33; DB 9; Length 15;
 Best Local Similarity 83.3%; Pred. No. 90; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 SEQ ID NO 416

QY 8 GRILCY 13
 DB 5 GRILCY 10

RESULT 22
 US-09-423-863-8
 Sequence 8, Application US/09423863
 Publication No. US20030054336A1

GENERAL INFORMATION:
 APPLICANT: Donie, Frederic
 APPLICANT: Faatz, Elke
 APPLICANT: Hoess, Eva

TITLE OF INVENTION: PROCESS FOR THE DETECTION OF HIV ANTIBODIES AND
 TITLE OF INVENTION: ANTIGENS USED IN IT
 FILE REFERENCE: BMID 9974 4638/OP/US-SZ
 CURRENT APPLICATION NUMBER: US/09/423-863

CURRENT FILING DATE: 2000-02-08
 EARLIER APPLICATION NUMBER: DE 19720914.9
 EARLIER FILING DATE: 1997-05-16
 EARLIER APPLICATION NUMBER: PCT/EP98/02816
 EARLIER FILING DATE: 1998-05-13

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 8
 LENGTH: 10
 TYPE: PRT

ORGANISM: Human immunodeficiency virus type 1

US-09-423-863-8

RESULT 23
 Query Match 34.8%; Score 31; DB 9; Length 10;
 Best Local Similarity 50.0%; Pred. No. 1.3e+02; Mismatches 2; Indels 0; Gaps 0;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 CKGRICITS 15
 DB 1 CSGKHCCTN 10

RESULT 23
 Query Match 34.8%; Score 31; DB 9; Length 10;
 Best Local Similarity 50.0%; Pred. No. 1.3e+02; Mismatches 2; Indels 0; Gaps 0;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 CKGRICITS 15
 DB 1 CSGKHCCTN 10

RESULT 23
 Query Match 34.8%; Score 31; DB 9; Length 10;
 Best Local Similarity 50.0%; Pred. No. 1.3e+02; Mismatches 2; Indels 0; Gaps 0;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 CKGRICITS 15
 DB 1 CSGKHCCTN 10

RESULT 23
 Query Match 34.8%; Score 31; DB 9; Length 10;
 Best Local Similarity 50.0%; Pred. No. 1.3e+02; Mismatches 2; Indels 0; Gaps 0;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 CKGRICITS 15
 DB 1 CSGKHCCTN 10

RESULT 23
 Query Match 34.8%; Score 31; DB 9; Length 10;
 Best Local Similarity 50.0%; Pred. No. 1.3e+02; Mismatches 2; Indels 0; Gaps 0;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 CKGRICITS 15
 DB 1 CSGKHCCTN 10

RESULT 24
 US-10-142-238A-49
 Sequence 49, Application US/10142238A
 Publication No. US20030087819A1

GENERAL INFORMATION:
 APPLICANT: Blelicki, John K.
 TITLE OF INVENTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES
 FILE REFERENCE: IB-1705
 CURRENT APPLICATION NUMBER: US/10/142-238A
 CURRENT FILING DATE: 2002-08-19

PRIOR APPLICATION NUMBER: US 60/2889, 944
 PRIOR FILING DATE: 2001-05-09
 NUMBER OF SEQ ID NOS: 84

SOFTWARE: PatentIn version 3.1
 SEQ ID NO 49
 LENGTH: 18
 TYPE: PRT

ORGANISM: ARTIFICIAL SEQUENCE
 FEATURE:
 NAME/KEY: PEPTIDE
 LOCATION: (1)..(18)
 OTHER INFORMATION: HUMAN GENETIC ORIGIN

US-10-142-238A-49

RESULT 25
 Query Match 34.8%; Score 31; DB 9; Length 18;
 Best Local Similarity 50.0%; Pred. No. 2.2e+02; Mismatches 4; Indels 0; Gaps 0;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 CKGRICITY 13
 DB 7 CRGRLVQY 14

RESULT 25
 US-09-423-863-7
 Sequence 7, Application US/09423863
 Publication No. US20030054336A1

GENERAL INFORMATION:
 APPLICANT: Donie, Frederic
 APPLICANT: Faatz, Elke
 APPLICANT: Hoess, Eva

TITLE OF INVENTION: PROCESS FOR THE DETECTION OF HIV ANTIBODIES AND
 TITLE OF INVENTION: ANTIGENS USED IN IT
 FILE REFERENCE: BMID 9974 4638/OP/US-SZ
 CURRENT APPLICATION NUMBER: US/09/423-863

CURRENT FILING DATE: 2000-02-08
 EARLIER APPLICATION NUMBER: DE 19720914.9
 EARLIER FILING DATE: 1997-05-16
 EARLIER APPLICATION NUMBER: PCT/EP98/02816
 EARLIER FILING DATE: 1998-05-13

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 416

RESULT 25
 Query Match 34.8%; Score 31; DB 9; Length 13;
 Best Local Similarity 55.6%; Pred. No. 1.6e+02; Mismatches 4; Indels 0; Gaps 0;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 4 WCKGRICTC 12
 DB 4 WPKCSGCTPC 12

; SEQ ID NO: 7
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-423-863-7

Query Match 33.7%; Score 30; DB 9; Length 10;
Best Local Similarity 55.6%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0;
Gaps 0;
Oy 6 CKGRCIYT 14
Db 1 CSGKHICCT 9

RESULT 26

US-09-572-404B-922
Sequence 922, Application US/09572404B
Publication No. US20030078374A1

GENERAL INFORMATION:

APPLICANT: Proteom, Ltd

TITLE OF INVENTION: Complementary peptide ligands from the human genome

FILE REFERENCE: Human patent

CURRENT APPLICATION NUMBER: US/09/572,404B

CURRENT FILING DATE: 2000-05-17

NUMBER OF SEQ ID NOS: 4203

SOFTWARE: ProtPatent version 1.0

SEQ ID NO: 922

LENGTH: 10

TYPE: PRT

ORGANISM: Homo Sapiens

FEATURE: peptide

OTHER INFORMATION: sequence located in MPPA at 11-20 and may interact with Sequence

US-09-572-404B-922

Query Match 33.7%; Score 30; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Oy 3 SWGC 6

Db 7 SWGC 10

LENGTH: 10

TYPE: PRT

ORGANISM: Homo Sapiens

FEATURE: peptide

OTHER INFORMATION: this patent.

US-09-572-404B-922

GENERAL INFORMATION:

APPLICANT: Wickham, Thomas J.

ROELVINK, Petrus W.

TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF

NUMBER OF SEQUENCES: 80

CORRESPONDENCE ADDRESS:

ADDRESSEE: Leydig, Voit & Mayer, Ltd.

STREET: Two Prudential Plaza - 49th Floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60601

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/969,192

FILING DATE: 01-Oct-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 9-455061

FILING DATE: 06-DEC-1999
APPLICATION NUMBER: US 9-130225
FILING DATE: 06-AUG-1998
APPLICATION NUMBER: US 8-701124
FILING DATE: 21-AUG-1996

ATTORNEY/AGENT INFORMATION:

NAME: Hafner, M. Daniel

REGISTRATION NUMBER: 41,826

REFERENCE/DOCKET NUMBER: 213564

INFORMATION FOR SEQ ID NO: 68:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 68:

US-09-969-192-68

Query Match 33.7%; Score 30; DB 10; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0;
Gaps 0;

Oy 6 CGRKLIYTS 15

Db 5 CRGDCFCCTS 14

RESULT 28

US-09-974-879-281

Sequence 281, Application US/09974879

Publication No. US20030028003A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: 125 Human Secreted Proteins

FILE REFERENCE: PZ2022

CURRENT APPLICATION NUMBER: US/09/974,879

CURRENT FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: US 60/239,893

PRIOR FILING DATE: 2000-10-13

PRIOR APPLICATION NUMBER: US 09/818,683

PRIOR FILING DATE: 2001-03-28

PRIOR APPLICATION NUMBER: US 09/305,736

PRIOR FILING DATE: 1999-03-05

PRIOR APPLICATION NUMBER: PCT/US98/23435

PRIOR APPLICATION NUMBER: US 60/064,911

PRIOR FILING DATE: 1997-11-07

PRIOR APPLICATION NUMBER: US 60/064,912

PRIOR FILING DATE: 1998-11-04

PRIOR APPLICATION NUMBER: US 60/064,983

PRIOR FILING DATE: 1997-11-07

PRIOR APPLICATION NUMBER: US 60/064,900

PRIOR FILING DATE: 1997-11-07

PRIOR APPLICATION NUMBER: US 60/064,988

PRIOR FILING DATE: 1997-11-07

PRIOR APPLICATION NUMBER: US 60/064,985

PRIOR FILING DATE: 1997-11-07

PRIOR APPLICATION NUMBER: US 60/064,987

PRIOR FILING DATE: 1997-11-07

PRIOR APPLICATION NUMBER: US 60/064,908

PRIOR FILING DATE: 1997-11-07

PRIOR APPLICATION NUMBER: US 60/064,984

PRIOR FILING DATE: 1997-11-07

PRIOR APPLICATION NUMBER: US 60/064,985

PRIOR FILING DATE: 1997-11-07

PRIOR APPLICATION NUMBER: US 60/064,989

PRIOR FILING DATE: 1997-11-17

PRIOR APPLICATION NUMBER: US 60/066,095

PRIOR FILING DATE: 1997-11-17

PRIOR APPLICATION NUMBER: US 60/066,090

PRIOR FILING DATE: 1997-11-17
 NUMBER OF SEQ ID NOS: 611
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 281
 LENGTH: 21
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-874-879-281

RESULT 29
 US-09-305-736-269
 Sequence 269, Application US/09305736
 Publication No. US200300808078A1
 GENERAL INFORMATION:
 APPLICANT: Feng et al. 125 Human Secreted Proteins
 TITLE OF INVENTION: 125 Human Secreted Proteins
 FILE REFERENCE: P2020P1
 CURRENT APPLICATION NUMBER: US/09/305,736
 CURRENT FILING DATE: 1999-05-05
 EARLIER APPLICATION NUMBER: PCT/US98/234435
 EARLIER FILING DATE: 1998-11-04
 EARLIER APPLICATION NUMBER: 60/064,911
 EARLIER FILING DATE: 1997-11-07
 EARLIER APPLICATION NUMBER: 60/064,912
 EARLIER FILING DATE: 1997-11-07
 EARLIER APPLICATION NUMBER: 60/064,983
 EARLIER FILING DATE: 1997-11-07
 EARLIER APPLICATION NUMBER: 60/064,990
 EARLIER FILING DATE: 1997-11-07
 EARLIER APPLICATION NUMBER: 60/064,991
 EARLIER FILING DATE: 1997-11-07
 EARLIER APPLICATION NUMBER: 60/064,992
 EARLIER FILING DATE: 1997-11-07
 EARLIER APPLICATION NUMBER: 60/064,993
 EARLIER FILING DATE: 1997-11-07
 EARLIER APPLICATION NUMBER: 60/064,994
 EARLIER FILING DATE: 1997-11-07
 EARLIER APPLICATION NUMBER: 60/064,998
 EARLIER FILING DATE: 1997-11-07
 EARLIER APPLICATION NUMBER: 60/064,989
 EARLIER FILING DATE: 1997-11-07
 EARLIER APPLICATION NUMBER: 60/064,987
 EARLIER FILING DATE: 1997-11-07
 EARLIER APPLICATION NUMBER: 60/064,908
 EARLIER FILING DATE: 1997-11-07
 EARLIER APPLICATION NUMBER: 60/064,908
 EARLIER FILING DATE: 1997-11-07
 EARLIER APPLICATION NUMBER: 60/064,985
 EARLIER FILING DATE: 1997-11-07
 EARLIER APPLICATION NUMBER: 60/064,984
 EARLIER FILING DATE: 1997-11-07
 EARLIER APPLICATION NUMBER: 60/064,984
 EARLIER FILING DATE: 1997-11-07
 EARLIER APPLICATION NUMBER: 60/064,989
 EARLIER FILING DATE: 1997-11-07
 EARLIER APPLICATION NUMBER: 60/066,095
 EARLIER FILING DATE: 1997-11-17
 EARLIER APPLICATION NUMBER: 60/066,090
 EARLIER FILING DATE: 1997-11-17
 NUMBER OF SEQ ID NOS: 612
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 269
 LENGTH: 21
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-305-736-269

RESULT 30
 US-09-999-724-93
 Sequence 93, Application US/99999724
 Publication No. US2003002235A1
 GENERAL INFORMATION:
 APPLICANT: WICKHAM, THOMAS J.
 APPLICANT: BROUGH, DOUGLAS E.
 TITLE OF INVENTION: VECTORS AND METHODS FOR GENE TRANSFER
 FILE REFERENCE: 212960
 CURRENT APPLICATION NUMBER: US/09/999,724
 CURRENT FILING DATE: 2001-10-24
 PRIOR APPLICATION NUMBER: US 09/101,751
 PRIOR FILING DATE: 1999-01-29
 PRIOR APPLICATION NUMBER: WO 96US19150
 PRIOR FILING DATE: 1996-11-27
 PRIOR APPLICATION NUMBER: US 08/700,846
 PRIOR FILING DATE: 1996-08-21
 PRIOR APPLICATION NUMBER: US 08/701,124
 PRIOR FILING DATE: 1996-08-21
 PRIOR APPLICATION NUMBER: US 08/563,368
 PRIOR FILING DATE: 1995-11-28
 NUMBER OF SEQ ID NOS: 94
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 93
 LENGTH: 14
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic
 US-09-999-724-93

Query Match 33.7%; Score 30; DB 9; Length 21;
 Best Local Similarity 71.4%; Pred. No. 3.5e+02; Mismatches 2;
 Matches 5; Conservative 0; Indels 0; Gaps 0;

Qy 1 LNSWCK 7
 | | | |
 Db 10 LRSWAK 16

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On protein - protein search, using sw model

Run on: June 5, 2003, 08:58:43 ; Search time 15 Seconds
(without alignments)
96.134 Million cell updates/sec

Title: US-09-605-573a-69_COPY_12_26

Perfect score: 89

Sequence: 1 LNSWGCKGRICIVTS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96114422 residues

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : PIR_73:*

1: PIR:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	30.3	13	S57367	T cell receptor V-J chain V-D-J r
2	27	30.3	20	S29335	Jacalin beta chain
3	26.5	29.8	15	S10386	Ig heavy chain J r
4	26	29.2	16	PC4416	5'BB kinase activa
5	26	29.2	19	1 EW5HAN	anconenin - Strept
6	25.5	28.7	17	S24570	Ig heavy chain J r
7	25.5	28.7	19	A58700	actagardine [valid
8	25	28.1	14	PH1306	Ig heavy chain DJ
9	25	28.1	15	S02381	probable membrane
10	24.5	27.5	14	S03530	Ig heavy chain J r
11	24	27.0	10	A59173	nuclese Bnl (EC 3
12	24	27.0	15	PH1318	Ig heavy chain DJ
13	24	27.0	19	PX0062	beta-galactoside-b
14	24	26.4	16	S03532	Ig heavy chain J r
15	23.5	26.4	16	D19021	Ig heavy chain J r
16	23	25.8	7	S57274	triacetylglycerol 11
17	23	25.8	11	PH1343	Ig heavy chain DJ
18	23	25.8	12	I6922	gene Bota protein
19	23	25.8	14	PH1639	Ig H chain V-D-J r
20	23	25.8	15	A56786	plimoyl-CoA synth
21	23	25.8	15	A5103	7 alpha-hydroxy-4-
22	23	25.8	16	A59046	alpha-conotoxin MI
23	23	25.8	18	S43958	Ig mu chain V-regi
24	23	25.8	19	C39305	neurotoxin Tx3 - s
25	23	25.3	17	S03531	Ig heavy chain J5
26	22	24.7	6	A61062	lucostakinin - mig
27	22	24.7	8	JS0315	leucokinin V - Mad
28	22	24.7	8	JS0316	leucokinin VI - Ma
29	22	24.7	8	JS0317	leucokinin VII - M

ALIGNMENTS

RESULT 1		ALIGNMENTS	
S57567	T cell receptor V-J Junctional alpha chain region - human (fragment)	Qy	1 LNSWGCKGRICVTS 15
C;Species: Homo sapiens (man)	C;Date: 19-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999	Db	2 LDYWG-EGTAVTVTS 15
C;Accession: S57567			
R;Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argaet, V.P.			
A;Description: T cell receptor repertoire for a viral epitope in humans is diversified by reference number: S57494			
A;Accession: S57567			
A;Status: preliminary			
A;Molecule type: mRNA			
A;Residues: 1-13 <BUR>			
A;Cross-references: EMBL:249949; NID:9887470; PIDN:CAA90220.1; PID:9887471			
A;Keywords: T-cell receptor			
Query Match 30.3%; Score 27; DB 2; Length 13;			
Best Local Similarity 100.0%; Pred. No. 6.4e+02; Mismatches 0; Indels 0; Gaps 0;			
Matches 4; Conservative 4;			
Qy 2 NSWG 5			
Db 5 NSWG 8			
RESULT 2		ALIGNMENTS	
S2635	jacalin beta chain - Artocarpus tonkinensis	Qy	1 LNSWGCKGRICVTS 15
C;Species: Artocarpus tonkinensis	C;Accession: S2635	Db	2 LDYWG-EGTAVTVTS 15
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997			
R;Ngoc, L.D.; Brillard, M.; Hoebeke, J. 1993			
Biochim. Biophys. Acta 1156, 219-222, 1993			
A;Title: The alpha- and beta-subunits of the jacalins are cleavage products from a 17-kD			
A;Reference number: S2635; MUID:93152601; PMID:8427879			
A;Accession: S2635			
A;Status: preliminary			
A;Molecule type: protein			
A;Residues: 1-20 <NGO>			
Query Match 30.3%; Score 27; DB 2; Length 20;			
Best Local Similarity 57.1%; Pred. No. 9.1e+02; Mismatches 4; Indels 1; Gaps 0;			
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;			
Qy 1 LNSWGCK 7			
Db 12 VGSWGAK 18			
RESULT 3		ALIGNMENTS	
S10386	Ig heavy chain J region (clone Re107) - little skate (fragment)	Qy	1 LNSWGCKGRICVTS 15
C;Species: Raja erinacea (little skate)	C;Accession: S10386	Db	2 LDYWG-EGTAVTVTS 15
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Aug-1996			
R;Harding, F.A.; Cohen, N.; Litman, G.W.			
Nucleic Acids Res. 18, 1015-1020, 1990			
A;Title: Immunoglobulin heavy chain gene organization and complexity in the skate, Raja			
A;Reference number: S08462; MUID:90192082; PMID:2107524			
A;Accession: S10386			
A;Molecule type: DNA			
A;Residues: 1-15 <HR>			
A;Cross-references: EMBL:X15124			
A;Keywords: heterotetramer; immunoglobulin			
Query Match 29.8%; Score 26.5%; DB 2; Length 15;			
Best Local Similarity 40.0%; Pred. No. 8.6e+02; Mismatches 6; Indels 1; Gaps 1;			
Matches 6; Conservative 4; Mismatches 4; Indels 1; Gaps 1;			
RESULT 4		ALIGNMENTS	
S24416	erbB kinase activator gamma, brain and thymus - rat (fragment)	Qy	1 LNSWGCKGRICVTS 15
C;Species: Rattus norvegicus (Norway rat)	C;Accession: S24416	Db	2 LDYWG-EGTAVTVTS 15
C;Date: 10-Dec-1997 #sequence_revision 10-Dec-1997 #text_change 02-Aug-2002			
R;Higashiyama, S.; Horikawa, M.; Yamada, K.; Ichino, N.; Nakano, N.; Nakagawa, T.; Mi			
J. Biochem. 122, 675-680, 1997			
A;Title: A novel brain-derived member of the epidermal growth factor family that interacts with the differentiation of MDA-MB-453 cells			
A;Reference number: JC5700; MUID:98006324; PMID:9348101			
A;Accession: S24416			
A;Status: nucleic acid sequence not shown			
A;Molecule type: mRNA			
A;Residues: 1-16 <HR>			
A;Cross-references: DDBJ:D89998; NID:92605635; PIDN:BAA23347.1; PID:92605636			
A;Experimental source: PC-12 cell			
C;Comment: This protein is a member of the epidermal growth factor family. It is functioning the differentiation of MDA-MB-453 cells.			
C;Superfamily: human ErBB kinase activator alpha, brain and thymus; EGF homology			
Query Match 29.2%; Score 26; DB 2; Length 16;			
Best Local Similarity 50.0%; Pred. No. 1.1e+03; Mismatches 1; Indels 0; Gaps 0;			
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;			
Qy 1 LNSWGCKG 8			
Db 9 INQLSCKG 16			
RESULT 5		ALIGNMENTS	
ENSMAN	ancovenin - Streptomyces sp. (strain A617P-2)	Qy	1 LNSWGCKGRICVTS 15
C;Species: Streptomyces sp.	C;Accession: A61284	Db	2 LDYWG-EGTAVTVTS 15
C;Date: 12-May-1994 #sequence_revision 19-May-1994 #text_change 19-May-1994			
C;Wakanishi, T.; Ueki, Y.; Shiba, T.; Kido, Y.; Motoki, Y.			
Tetrahedron Lett. 26, 665-668, 1985			
A;Title: The structure of ancovenin, a new peptide inhibitor of angiotensin I converting enzyme number: A61284			
A;Reference number: A61284			
A;Accession: A61284			
A;Molecule type: protein			
A;Residues: 1-19 <WAK>			
C;Superfamily: cinnamycin precursor			
C;Keywords: antibiotic; lanthanide			
C;Description: sp-(2S,6R)-3-methyl-lanthanone (Cys-Thr) #status experimental			
F,4-14/cross-link: sp-(2S,6R)-3-methyl-lanthanone (Ser-Cys) #status experimental			
F,4-14/cross-link: sp-(2S,3S,6R)-3-methyl-lanthanone (Cys-Thr) #status experimental			
F,5,11/cross-link: (2S,3S,6R)-3-methyl-lanthanone (Ser) #status experimental			
F,6/Modified site: dehydroalanine (Ser) #status experimental			
Query Match 29.2%; Score 26; DB 1; Length 19;			
Best Local Similarity 50.0%; Pred. No. 1.2e+03; Mismatches 3; Indels 0; Gaps 0;			
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;			
Qy 3 SWGCKG 8			
Db 11 TWSCDG 16			
RESULT 6		ALIGNMENTS	
S24570	Ig heavy chain J region - channel catfish	Qy	1 LNSWGCKGRICVTS 15
C;Species: Ictalurus punctatus (channel catfish)	C;Accession: S24570	Db	2 LDYWG-EGTAVTVTS 15
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999			
R;Wilson, M.R.			
C;Comment: submitted to the EMBL Data Library, March 1992			
A;Reference number: S24570			
A;Accession: S24570			

A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-17 <WIG>
 A;Cross-references: EMBL:X65182; NID:964015; PIDN:CAA6293.1; PID:964016
 C;Keywords: heterotetramer; immunoglobulin
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin

Query Match 28.7%; Score 25.5; DB 2; Length 17;
 Best Local Similarity 50.0%; Pred. No. 1.4e+03; Pred. No. 1.4e+03;
 Matches 6; Conservative 1; Mismatches 4; Indels 1; Gaps 1;
 Qy 4 WGCKGRICIVS 15
 ||| : |||
 Db 7 WG-KGTAVTVTS 17

RESULT 7
 A58700 actagardine [validated] - "Actinoplanes liguriae"
 N;Alternate names: gardimycin
 C;Species: "Actinoplanes liguriae"
 A;Note: ATCC 31048
 C;Date: 16-Jan-1998 #sequence_revision 23-Jan-1998 #text_change 15-Sep-2000
 C;Accession: A58700; A58701
 R;Zimmermann, N.; Jung, G. 1997
 A;Title: The three-dimensional solution structure of the lantibiotic murein-biosynthesis
 A;Reference: number: A58700; MUID:97363218; PMID:9219543
 A;Accession: A58700
 A;Molecule type: protein
 A;Residues: 1-19 <ZIM>
 A;Note: the assignment of residues 1-ser and 6-Cys are based on model studies
 R;Zimmermann, N.; Metzger, J.W.; Jung, G. 1995
 A;Title: The tetracyclic lantibiotic actagardine. (1)H-NMR and (13)C-NMR assignments and
 A;Reference number: A58701; MUID:95255286; PMID:7737178
 A;Accession: A58701
 A;Molecule type: protein
 A;Residues: X, 2-5, X', 7-19 <Z12>
 A;Note: residues 1 and 6, indicated as 'X', are serine and cysteine, but which is in whi
 R;Zimmermann, N.; Jung, G.
 C;Submitted to the Brookhaven Protein Data Bank, May 1997
 A;Contents: Annotation; conformation and cross-link assignments by (1)H- and (13)C-NMR,
 C;Comment: The antibiotic activity arises through inhibition of a glycopeptide transglyc
 C;Keywords: antibiotic; lanthionine
 F;1-6/cross-link: sn-1S,6R-lanthionine (Ser-Cys) #status experimental
 F;7-12/cross-link: (2S,3S,6R)-3-methyl-lanthionine (Thr-Cys) #status experimental
 F;9-17/cross-link: (2S,3S,6R)-3-methyl-lanthionine (Thr-Cys) #status experimental
 F;14-19/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Thr-Cys) #status experimental

Query Match 28.7%; Score 25.5; DB 2; Length 19;
 Best Local Similarity 31.2%; Pred. No. 1.5e+03;
 Matches 5; Conservative 2; Mismatches 4; Indels 5; Gaps 1;
 Qy 2 NSNGCK----GRIC 12
 ||| : |||
 Db 2 SGWVCTTIECGTIVC 17

RESULT 8
 PH1306
 19 heavy chain DJ region (clone C95-100) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993. #text_change 07-May-1999
 C;Accession: PH1306
 R;Wasserman, R.; Galil, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
 J;Exp. Med. 176, 1575-1581, 1992
 A;Title: Predominance of fetal type DJH Joining in young children with B precursor lymph
 A;Reference number: PH1302; MUID:93094761; PMID:1460419
 A;Accession: PH1306
 A;Molecule type: DNA

RESULT 9
 S02381
 probable membrane antigen C11 - human herpesvirus 4 (fragment)
 C;Species: human herpesvirus 4, Epstein-Barr virus
 C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 08-Oct-1999
 C;Accession: S02381
 R;Walls, D.; Gammie, F.
 EMBO J. 7, 1191-1196, 1988
 A;Title: The expression of novel antigens from the Epstein-Barr virus large internal
 A;Reference number: S02381; MUID:88296424; PMID:2841116
 A;Accession: S02381
 A;Molecule type: DNA
 A;Residues: 1-15 <WAL>
 A;Cross-references: EMBL:X07814; NID:959167; PIDN:CAA30673.1; PID:9330013
 C;Keywords: membrane protein; surface antigen

Query Match 28.1%; Score 25; DB 2; Length 14;
 Best Local Similarity 66.7%; Pred. No. 1.5e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 4 WGCKGR 9
 ||| : |||
 Db 6 WGKSGR 11

RESULT 10
 S03530
 Ig heavy chain J region (JH-4) - African clawed frog
 C;Species: Xenopus laevis (African clawed frog)
 C;Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 21-Jul-2000
 C;Accession: S03530
 R;Schwager, R.; Grossberger, D.; du Pasquier, L.
 EMBO J. 7, 2405-2415, 1988
 A;Title: Organization and rearrangement of immunoglobulin M genes in the amphibian xe
 A;Reference number: S01158; MUID:89052653; PMID:2903824
 A;Accession: S03530
 A;Molecule type: DNA
 A;Residues: 1-14 <SCH>
 A;Cross-references: EMBL:X14918; NID:964805; PIDN:CAA3043.1; PID:91334657

Query Match 27.5%; Score 24.5; DB 2; Length 14;
 Best Local Similarity 41.7%; Pred. No. 1.7e+02;
 Matches 5; Conservative 3; Mismatches 3; Indels 1; Gaps 1;
 Qy 4 WGCKRICKVTS 15
 ||| : |||
 Db 4 WG-QGTVTVTS 14

RESULT 11
 A59173
 nuclelease Bhl (EC 3.1.-.-) - Basidiobolus haptosporus (fragment)
 C;Species: Basidiobolus haptosporus
 C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
 C;Accession: A59173
 R;Desai, N.; Shankar, V.
 J;Exp. Med. 176, 1575-1581, 1992
 A;Title: Predominance of fetal type DJH Joining in young children with B precursor lymph
 A;Reference number: A59173
 A;Accession: A59173
 A;Status: preliminary

A; Molecule type: protein
 A; Residues: 1-10 <DPS>
 A; Note: extracellular, single-strand-specific nuclease
 C; Keywords: hydrolase

Query Match 27.0%; Score 24; DB 2; Length 10;
 Best Local Similarity 37.5%; Pred. No. 1.5e+03;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy 4 WGCKGRIT 11
 Db 1 WGLGLHLL 8

RESULT 12

PH1318 Ig heavy chain DJ region (clone C527-121) - human (fragment)

C; Species: Homo sapiens (man)
 C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C; Accession: PH1318
 R; Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
 J; Exp. Med. 176: 1577-1581, 1992
 A; Title: predominance of fetal type DJH joining in young children with B precursor lymph
 A; Reference number: PH1302; MUID:93094761; PMID:1460419
 A; Accession: PH1318
 A; Molecule type: DNA
 A; Residues: 1-15 <WAS>
 C; Keywords: heterotetramer; immunoglobulin

Query Match 27.0%; Score 24; DB 2; Length 15;
 Best Local Similarity 57.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 11 ICYT 14
 Db 2 VCYT 5

RESULT 13

PX0062 beta-galactoside-binding lectin - Caenorhabditis elegans (fragment)

C; Species: Caenorhabditis elegans (fragment)
 C; Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 26-May-2000
 C; Accession: PX0062
 R; Hirabayashi, J.; Satoh, M.; Ohyama, Y.; Kasai, K.
 J; Biochem. 111, 553-555, 1992
 A; Title: Purification and characterization of beta-galactoside-binding proteins from Caen
 A; Reference number: PX0062; MUID:9234337; PMID:1639749
 A; Accession: PX0062
 A; Molecule type: protein
 A; Residues: 1-19 <HIL>
 C; Superfamily: lactose-binding lectin L-36

Query Match 27.0%; Score 24; DB 2; Length 19;
 Best Local Similarity 50.0%; Pred. No. 2.5e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 2 NSWGKGR 9
 Db 10 NEWGNER 17

RESULT 14

S03532 19 heavy chain J region (JH-7) - African clawed frog
 C; Species: Xenopus laevis (African clawed frog)

C; Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 20-Jun-2000
 C; Accession: S03532
 R; Schwager, J.; Grossberger, D.; du Pasquier, L.
 EMB J. 7, 2409-2415, 1988

A; Title: Organization and rearrangement of immunoglobulin M genes in the amphibian Xenop
 A; Reference number: S0118; MUID:89052653; PMID:2003824
 A; Accession: S03532

A; Molecule type: DNA

A; Residues: 1-16 <SCB>

A; Cross-references: EMBL:X14918; NID:964805; PIDN:CAA33046_1; PID:91334660

A; Note: the authors translated the codon AAC for residue 1 as Asp

C; Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 26.4%; Score 23.5; DB 2; Length 16;
 Best Local Similarity 41.7%; Pred. No. 2.6e+03;
 Matches 5; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

Oy 4 WGCKGRICYTS 15
 Db 6 WG-QGTMVTVTS 16

RESULT 15

D49021 Ig heavy chain J7 region - African clawed frog
 C; Species: Xenopus laevis (African clawed frog)

C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
 C; Accession: D49021
 R; Haile, R.N.; Amanya, C.T.; Suzuki, D.; Litman, G.W.
 J; Exp. Med. 171, 1721-1737, 1990
 A; Title: Eleven distinct V-H gene families and additional patterns of sequence variation
 A; Reference number: A47624; MUID:90237760; PMID:2110243
 A; Accession: D49021
 A; Status: preliminary; not compared with conceptual translation

A; Molecule type: mRNA

A; Residues: 1-16 <HIL>

C; Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 26.4%; Score 23.5; DB 2; Length 16;
 Best Local Similarity 41.7%; Pred. No. 2.6e+03;
 Matches 5; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

Oy 4 WGCKGRICYTS 15
 Db 6 WG-QGTMVTVTS 16

RESULT 16

S57274 triacylglycerol lipase (EC 3.1.1.3) - Psychrobacter immobilis (fragment)

C; Species: Psychrobacter immobilis
 C; Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 03-Nov-1995
 C; Accession: S57274
 R; Arpigny, J.I.; Feller, G.; Gerday, C.
 Biochim. Biophys. Acta 1293, 103, 1995
 A; Title: Corrigendum to "Cloning, sequence and structural features of a lipase from t
 A; Reference number: S57274; MUID:95359197; PMID:7632728
 A; Accession: S57274
 A; Status: preliminary

A; Molecule type: DNA
 A; Residues: 1-7 <ARP>
 A; Cross-references: EMBL:X67712
 C; Keywords: carboxylic ester hydrolase

Query Match 25.8%; Score 23; DB 2; Length 7;
 Best Local Similarity 57.1%; Pred. No. 2.8e+05;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 4 WGCKGR 10
 Db 1 WGDQDQI 7

RESULT 17

PH1343 19 heavy chain DJ region (clone C100-91) - human (fragment)

C; Species: Homo sapiens (man)
 C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C; Accession: PH1343

R; Wasserman, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992

A; Title: Predominance of fetal type DJH joining in young children with B precursor lymphocytes
A; Accession: PH1302; MUID:93094761; PMID:1460419

A; Molecule type: DNA

A; Residues: 1-11 <WKS>

C; Keywords: heterotetramer; immunoglobulin

Query Match 25.8%; Score 23; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNSWG 5
Db 4 LDNWG 8

RESULT 18
I46922

gene Bota protein - bovine (fragment)
C; Species: Bos primigenius taurus (cattle)
C; Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 05-Nov-1999
C; Accession: I46922

A; Title: Transmembrane and cytoplasmic domain sequences demonstrate at least two expressed
A; Reference number: I46921; MUID:93052564; PMID:1428011

A; Accession: I46922

A; Status: Preliminary; translated from GB/EMBL/DBJ

A; Molecule type: mRNA

A; Residues: 1-12 <ELH>

A; Cross-references: GB:547738; NID:9258999; PIDN:AAB23972.1; PID:9259000

C; Genetics: A

A; Gene: Bota2

Query Match 25.8%; Score 23; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 3e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 10 IICYT 14
Db 2 LICKS 6

RESULT 19
I46923

Ig H chain V-D-J region (clone B-less 230) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C; Accession: PH1639

R; Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993

A; Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A; Reference number: PH1580; MUID:93301609; PMID:8315387

A; Accession: PH1639

A; Molecule type: DNA

A; Residues: 1-14 <LEV>

A; Experimental source: bone marrow pre-B lymphocyte

C; Keywords: immunoglobulin

Query Match 25.8%; Score 23; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 8 GRITCY 13
Db 1:i:1 7 GVILCY 12

RESULT 20
A56786

Palmitoyl-CoA synthase - *Bacillus sphaericus* (fragment)

Query Match 25.8%; Score 23; DB 2; Length 16;

C; Species: *Bacillus sphaericus*
C; Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 18-Aug-1995
C; Accession: A56786

R; Ploux, O.; Soulard, P.; Marquet, A.; Gloeckler, R.; Lemoine, Y.
Biochem. J. 287, 685-690, 1992

A; Title: Investigation of the first step of biotin biosynthesis in *Bacillus sphaericus*
A; Reference number: A56786; MUID:93075017; PMID:1445332

A; Status: preliminary

A; Molecule type: protein

A; Residues: 1-15 <PLQ>

A; Experimental source: *Bacillus sphaericus* protein overexpressed in *Escherichia coli*
A; Note: sequence extracted from NCBI backbone (NCBIP:117639)

C; Genetics: A

A; Gene: biow

C; Keywords: biotin biosynthesis; homodimer

Query Match 25.8%; Score 23; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 3e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 10 IICYT 14
Db 2 LICKS 6

RESULT 21
A5103

7 alpha-hydroxy-4-cholestene-3-one 12 alpha-hydroxylase, cytochrome P450 12alpha, HCO C; Species: Oryctolagus cuniculus (domestic rabbit)
C; Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 03-Mar-1995
C; Accession: A45103

R; Ishida, H.; Nosiro, M.; Okuda, K.; Coon, M.J.
J. Biol. Chem. 268, 21319-21323, 1992

A; Title: Purification and characterization of 7 alpha-hydroxy-4-cholestene-3-one 12 alpha-hydroxylase
A; Reference number: A5103; MUID:93016066; PMID:1400444

A; Accession: A5103

A; Status: preliminary

A; Molecule type: protein

A; Residues: 1-15 <PSH>

A; Experimental source: liver microsomes

A; Note: sequence extracted from NCBI backbone (NCBIP:116791)

Query Match 25.8%; Score 23; DB 2; Length 15;
Best Local Similarity 37.5%; Pred. No. 3e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 4 WGCHGRII 11
Db 3 WGLLGALL 10

RESULT 22
A59046

alpha-conotoxin MII - cone shell (*Conus magus*)
C; Species: *Conus magus* (magus cone)
C; Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C; Accession: A59046

R; Cartier, G.E.; Yoshikami, D.; Gray, W.R.; Luo, S.; Olivera, B.M.; McIntosh, J.M.
J. Biol. Chem. 271, 7522-7528, 1996

A; Title: A new alpha-conotoxin which targets alpha3beta2 nicotinic acetylcholine receptors
A; Reference number: A59046; MUID:96205934; PMID:8631783

A; Accession: A59046

A; Status: preliminary

A; Molecule type: protein

A; Residues: 1-16 <CAR>

C; Superfamily: alpha-conotoxin

F; 1-16 Product: alpha-conotoxin MII #status experimental <MAY>
F; 2-8-3-16 Disulfide bonds: #status experimental
F; 16/Modified site: amidated carboxyl end (Cys) #status experimental

Best Local Similarity 33.3%; Pred. No. 3.1e+03; Indels 0; Gaps 0; Matches 3; Conservative 2; Mismatches 0;

Y 5 GCKGRICY 13
|| :;
1 GCCSNWCH 9

RESULT 23

Best Local Similarity 49.9%; Pred. No. 3.9e+03; Indels 0; Gaps 0; Matches 3; Conservative 2; Mismatches 0;

Y 443958
| :;
1 GCKGRICY 13

Query Match 25.8%; Score 23; DB 2; Length 18; C:Species: Homo sapiens (man)
C:Accession: S43958
C:Date: 20-Oct-1994 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
C:Residues: WAGNER, S.D.; WILLIAMS, G.T.; LARSON, T.; NEUBERGER, M.S.; KITAMURA, D.; RAJEWSKY, K.; NUCLEIC ACIDS RES. 22, 1389-1393, 1994
A:Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice.
A:Reference number: S43956; MUID:94248036; PMID:8190629

Accession: S43958
A;Molecule type: DNA
C;Keywords: immunoglobulin V region; immunoglobulin homology
C;Superfamily: heterotrimer; immunoglobulin

RESULT 24

Best Local Similarity 41.8%; Pred. No. 3.9e+03; Indels 0; Gaps 0; Matches 3; Conservative 2; Mismatches 0;

Y 4439305
| :;
1 GCKGRICY 13

Query Match 25.8%; Score 23; DB 2; Length 18; C:Species: Immunoglobulin
C:Accession: C39305
C:Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 07-Feb-1997
C:Residues: PHONEUTRIA NIGRIVENTER
C:Keywords: neurotoxin Tx3 - spider (Phoneutria nigriventer) (fragment)

Accession: C39305
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-18 <REZ>
A;Keywords: neurotoxin

Query Match 25.8%; Score 23; DB 2; Length 19; C:Species: Leucophaea maderae (Madeira cockroach)
C:Accession: JS0315
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C:Residues: Leucokinin V - Madeira cockroach
C:Keywords: Leucophaea maderae (Madeira cockroach)

Accession: JS0315
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-17 <REZ>
A;Keywords: Leucokinin V - Madeira cockroach

RESULT 25

Best Local Similarity 49.9%; Pred. No. 3.9e+03; Indels 0; Gaps 0; Matches 3; Conservative 2; Mismatches 0;

Y 443931
| :;
1 GCKGR 5

Query Match 25.8%; Score 23; DB 2; Length 19; C:Species: Xenopus laevis (African clawed frog)
C:Accession: S03531; C49021
C:Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 20-Jun-2000
C:Residues: R; SCHWADER, J.; GROSSBERGER, D.; DU PASQUIER, L.
C:Keywords: Ig heavy chain J5 region - African clawed frog

Accession: S03531
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-17 <REZ>
A;Keywords: Cross-references: EMBL:X14918; NID:964805; PID:CAA33044.1; PID:91334658
R; HAIRE, R.N.; AMENIYA, C.T.; SUZUKI, D.; LITMAN, G.W.
J. EXP. MED. 171, 1721-1737, 1990

RESULT 26

Best Local Similarity 41.8%; Pred. No. 3.9e+03; Indels 0; Gaps 0; Matches 5; Conservative 2; Mismatches 4;

Y 4439308
| :;
1 GCKGR 5

Query Match 24.7%; Score 22; DB 2; Length 6; C:Species: Locusta migratoria (migratory locust)
C:Accession: A61068
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 08-Dec-1995
C:Residues: SCHOELS, L.; HOLMAN, G.M.; PROOST, P.; VAN DAMME, J.; HAYES, T.K.; DE LOOF, A.
C:Keywords: Locustakinin - migratory locust
Regul. Pept. 37, 49-57, 1992
A;Title: Locustakinin, a novel myotrophic peptide from Locusta migratoria, isolation, A;Reference number: A61068; MUID:92262851; PMID:1585017

Accession: A61068
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-6 <SCH>
A;Keywords: amidated carboxyl end; cephalomyotrophic peptide; neuropeptide F; 5/Modified site: amidated carboxyl end (Gly) #status experimental

RESULT 27

Best Local Similarity 75.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0; Matches 3; Conservative 1; Mismatches 0;

Y 2 NSWG 5
| :;
1 GCKGR 5

Query Match 24.7%; Score 22; DB 2; Length 6; C:Species: Leucophaea maderae (Madeira cockroach)
C:Accession: JS0315
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C:Residues: Leucokinin V - Madeira cockroach
C:Keywords: Leucophaea maderae (Madeira cockroach)

Accession: JS0315
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <REZ>
A;Keywords: Leucokinin V - Madeira cockroach

RESULT 28

Best Local Similarity 75.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0; Matches 3; Conservative 1; Mismatches 0;

Y 2 NSWG 5
| :;
1 GCKGR 5

Query Match 24.7%; Score 22; DB 2; Length 8; C:Species: Leucophaea maderae (Madeira cockroach)
C:Accession: JS0316
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C:Residues: LEUCOPHAEA MADERAE (MADEIRA COCKROACH)
C:Keywords: Leucophaea maderae (Madeira cockroach)

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
 C;Accession: JS0316

R;Holman, G.M.; Cook, B.J.; Nachman, R.J.

Comp. Biochem. Physiol. C 88, 2730, 1987

A;Title: Isolation, primary structure, and synthesis of leucokinins V and VI: myotropic

A;Reference number: JS0315

A;Accession: JS0316

A;Molecule type: protein

A;Residues: 1-8 <H02>

C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile act

C;Keywords: amidated carboxyl end; cephalomyotropic peptide; pyroglutamic acid

F;8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match

Best Local Similarity 24.7%; Score 22; DB 2; Length 8;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NSWG 5

Db 5 HSWG 8

RESULT 29

JS0317

leucokinin VII - Madeira cockroach

C;Species: Leucophaea maderae (Madeira cockroach)

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000

C;Accession: JS0317

R;Holman, G.M.; Cook, B.J.; Nachman, R.J.

Comp. Biochem. Physiol. C 88, 31-34, 1987

A;Title: Isolation, primary structure and synthesis of leucokinins VII and VIII: the fin

A;Reference number: JS0317

A;Accession: JS0317

A;Molecule type: protein

A;Residues: 1-8 <H01>

C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile act

C;Keywords: amidated carboxyl end; cephalomyotropic peptide

F;8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match

24.7%; Score 22; DB 2; Length 8;

Best Local Similarity 75.0%; Pred. No. 2.8e+05; Length 8;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NSWG 5

Db 5 SSWG 8

RESULT 30

A2244

adipokinetic hormone - boilworm

N;Alternate names: Hec-AKH

C;Species: Helicthis zea (boilworm, corn earworm, tomato fruitworm)

C;Date: 31-Mar-1988 #sequence_revision 23-Mar-1995 #text_change 31-Oct-1997

C;Accession: A2244

R;Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridgway

Biochem. Biophys. Res. Commun. 135, 622-628, 1986

A;Title: Isolation and primary structure of a peptide from the corpora cardiaca of Helic

A;Reference number: A2244; MUID:86186794; PMID:3964263

A;Accession: A2244

A;Molecule type: protein

A;Residues: 1-9 <JAF>

C;Superfamily: adipokinetic hormone

C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic

F;9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match

24.7%; Score 22; DB 2; Length 9;

Best Local Similarity 75.0%; Pred. No. 2.8e+05; Length 9;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NSWG 5

Db 6 :||| SSWG 9

Search completed: June 5, 2003, 09:00:02

Job time : 18 secs

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OM protein - protein search, using sw model

Run on: June 5, 2003, 08:58:43 ; Search time 11 Seconds

Scoring table: BLOSUM62 ; (without alignments)
56.559 Million cell updates/sec

Title: US-09-605-573A-69_COPY_12_26

Perfect score: 89

Sequence: 1 LNSNGCKGRICVTS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 1147

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : SwissProt_40.0

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	%	Match	Length	DB	ID	Description
1	27	30.3	8	1	LCK3_1 LEUMA	P21140	leucophaea	
2	27	30.3	8	1	LCK3_2 LEUMA	P21142	leucophaea	
3	27	30.3	20	1	LECI_1 ARTINA	P18671	artocarpus	
4	26	29.2	19	1	DURE_1 ARTINA	P26503	streptomyce	
5	26	29.2	19	1	LANC_1 STRO	P38655	streptomyce	
6	25.5	28.7	19	1	LANA_1 ACTING	P56650	actinoplane	
7	23	25.8	12	1	CXL2_1 CONMR	P58809	conus maximo	
8	23	25.8	16	1	CXA2_1 CONNA	P56635	conus magus	
9	23	25.8	19	1	TX3_1 PHONT	P31010	phoneutria	
10	22	24.7	6	1	LOK1_1 LOOMI	P41491	locusta mig	
11	22	24.7	8	1	LCK2_1 LEUMA	P21141	leucophaea	
12	22	24.7	8	1	LCK5_1 LEUMA	P21143	leucophaea	
13	22	24.7	8	1	LCK6_1 LEUMA	P19987	leucophaea	
14	22	24.7	8	1	LCK6_2 LEUMA	P19988	leucophaea	
15	22	24.7	8	1	LCK7_1 LEUMA	P19989	leucophaea	
16	22	24.7	11	1	CEP1_1 ACHEU	P22790	achatinina fu	
17	22	24.7	15	1	LCK_1 DRONE	P81829	drosophilida	
18	22	24.7	18	1	GONE_1 ACAGO	P82358	cartharsius	
19	22	24.7	19	1	SCX6_1 TTIBA	P56610	tityus bahi	
20	22	24.7	20	1	LECC3_1 ARTIN	P18673	artocarpus	
21	21	23.6	8	1	LCK8_1 LEUMA	P19980	leucophaea	
22	21	23.6	17	1	TAC1_1 TACGI	P22790	achatinina fu	
23	21	23.6	17	1	TAC2_1 TACGI	P81829	drosophilida	
24	20	22.5	11	1	COL1_1 CONMR	P58807	conus marmo	
25	20	22.5	12	1	TIN3_1 HOPTI	P82653	hoploblastac	
26	20	22.5	13	1	CXL4_1 CONMR	P58810	conus marmo	
27	20	22.5	14	1	SNS1_1 MYOSC	P20750	myoxocephalo	
28	20	22.5	14	1	CX1B_1 COMBI	P31085	alligator	
29	20	22.5	15	1	ISOT1_1 CYPCA	P58624	conus betul	
30	19	21.3	9	1	OXYT1_1 RAJCL	P42993	cyprinus ca	
31	19	21.3	9	1	TIN4_1 HOPTI	P82994	raja clavat	
32	19	21.3	11	1	TIN4_2 HOPTI	P82654	hoploblastac	
33	19	21.3	12	1	OXAL1_1 CONMR	P09983	conus imper	

RESULT 1

ALIGNMENTS

P11760 arbacia pun
P45661 leiurolia qui
P55025 chlorobius
P81666 pinus pinus
P14215 limulus pol
P14216 limulus pol
P58811 conus tulip
P80406 verticilliu
P99505 canis famili
P18110 romalea mic
P1385 caranxius m
P16353 heliothis 2
P57104 rana tempor
P01560 escherichia
P18691 thunnum alb
P20728 calotropis
P30426 bothrops in
P10939 nauphoeta c
P58925 zea mays (m
P58927 conus pena
P01589 anolis caro
P01198 camellia dro
P55961 vitis sativ
P21654 vespa basal
P58842 conus quer
P56640 conus aulic
P80614 carreata car
P56633 conus aulic
P56641 conus aulic
P23002 azotobacter
P08352 rana rugosa
P01202 equus cabal
P01206 scylliorhinu
P52664 azotobacter
P80527 fasciola he
P18676 maculura pom
P18677 maculura pom
P20424 actinobacil
P42992 scylliorhinu
P42999 squamus aca
P42999 scylliorhinu
P22879 bufonidae
P80027 octopus vul
P32878 oxyctolagus
P33000 squamus aca
P02728 homo sapien
P11_1 TINI_1 HOPTI
P22651 hoploblastac
P22790 cyprinus ca
P80026 white spot
P56917 rana tempor
P41122 photobacter
P03056 citrobacter
P03054 salmonella
P99505 canis famili
P8846 conus texti
P82006 white spot
P56917 rana tempor
P41122 photobacter
P03056 citrobacter
P03054 salmonella
P99505 canis famili
P81358 clostridium
P42559 manduca sex
P19181 lumbriucus
P80629 zea mays (m
P14458 mustela vis
P14461 orctocelagus
Q10756 naja sputat

us-09-605-5/3a-69_copy_12_20.1sf

Query Match	28.7%	Score 25.5; DB 1; Length 19;	RN [2]
Best Local Similarity	31.2%	Pred. No. 3.7e+02;	RN
Matches	5;	Mismatches 4;	STRUCTURE BY NMR.
QY	2	NSWGCK---GRTIC 12	MEDLINE=98062282; PubMed=9398298;
DB	2	: : :	Shon K.-J., Koerner S.C., Rivier J.E., Olivera B.M., McIntosh J.M.;
		SGWVCTLTLIECGTVIC 17	"Three-dimensional solution structure of alpha-conotoxin MII, an alpha/beta2 neuronal nicotinic acetylcholine receptor-targeted ligand";
RESULT 7			RT [3]
CX13_CONMR		STANDARD;	RT
ID		PRT; 12 AA.	RL
AC			STRUCTURE BY NMR.
PS8809;			RT
DT	15-JUN-2002 (Rel. 41, Created)		RT
DT	15-JUN-2002 (Rel. 41, Last sequence update)		RT
DT	15-JUN-2002 (Rel. 41, Last annotation update)		RT
DE	Lambda-conotoxin CMX.		RL
OS	Conus marmoreus (Marble cone).		Biochemistry 36:15693-15700(1997).
OC	Eukaryota; Metazoa; Mollusca 2.		
OC	Neogastropoda; Conoidea; Conidae; Conus.		
OX	NCBI_TAXID=42752;		
RN	[1]	SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.	
RP			
TISSUE=Venom;			
MEDLINE=20564325; PubMed=10988292;			
RA	Balaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M.,		
RA	Seow K.T., Bay B.-H.		
RT	"Lambda-conotoxins, a new family of conotoxins with unique disulfide pattern and protein folding. Isolation and characterization from the venom of Conus marmoreus."		
RT	J. Biol. Chem. 275:39516-39522(2000).		
CC	-1- FUNCTION: Inhibits the neuronal noradrenaline transporter.		
CC	-1- SUBCELLULAR LOCATION: Secreted.		
CC	-1- TISSUE SPECIFICITY: Expressed by the venom duct.		
CC	-1- MASS SPECTROMETRY: MW=1262.77; MW_ERP=0.07; METHOD=Electrospray.		
CC	-1- SIMILARITY: BELONGS TO THE CHI/LAMBDA-CONOTOXIN FAMILY.		
KW	Neurotoxin; Toxin; Hydroxylation.		
FT	DISULFID	21-OCT-98.	
FT	DISULFID	PDB: 1M1C; 13-JAN-99.	
FT	MOD_RES	Postsynaptic neurotoxin; Neurotoxin; Toxin;	
FT	SEQUENCE	Acetylcholine receptor inhibitor; Amidation; 3D-structure.	
SO	SEQUENCE 12 AA; 1251 MW; 277AAE2422D5AC8 CRK64;		
Query Match	25.8%	Score 23; DB 1; Length 12;	RN
Best Local Similarity	50.0%	Pred. No. 6.2e+02;	RX
Matches	4;	Mismatches 4;	STRUCTURE BY NMR.
QY	6	GKGRIC 13	MEDLINE=9219603; PubMed=1801316;
DB	1	:	Shon K.-J., Koerner S.C., Rivier J.E., Olivera B.M., McIntosh J.M.;
	3	CCGVSFCY 10	"Isolation of neurotoxic peptides from the venom of the 'armed' spider Phoneutria nigriventer (Brazilian armed spider)."
RESULT 8			
CX12_COMMA		STANDARD;	
ID		PRT; 16 AA.	
AC			
P56636;			
DT	15-DEC-1998 (Rel. 37, Created)		
DT	15-DEC-1998 (Rel. 37, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Alpha-conotoxin MII (M2).		
OS	Conus magus (Magus cone).		
OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;		
OC	Neogastropoda; Conoidea; Conidae; Conus.		
OX	NCBI_TAXID=6492;		
RN	[1]	SEQUENCE, AND SYNTHESIS.	
RC	TISSUE=Venom;		
RX	MEDLINE=96205934; PubMed=8631783;		
RA	Carter G.E., Yoshikami D., Gray W.R., Luo S., Olivera B.M.,		
RA	McIntosh J.M.;		
RT	"A new alpha-conotoxin which targets alpha3beta2 nicotinic acetylcholine receptors";		
RT	J. Biol. Chem. 271:7522-7528(1996).		
SO	SEQUENCE 19 AA; 2244 MW; 3214E89CF10F7587 CRC64;		

Query Match		25.8%	Score 23;	DB 1;	Length 19;	AMIDATION	
Best Local Similarity		80.0%	Pred. No. 9.4e+02;	Indels 1;	0; Gaps 0;	Matches 4; Conservative 0; Mismatches 0;	
Qy	Db	5 GCKGR 9	1 GCGGR 5				
RESULT 10							
LCK1_LOCMI	STANDARD;		PRT;	6 AA.			
ID LCK1_LOCMI							
AC PA1491;							
DT 01-NOV-1995 (Rel. 32, Created)							
DT 01-NOV-1995 (Rel. 32, Last sequence update)							
DE 15-JUL-1998 (Rel. 36, Last annotation update)							
Locusta migratoria (Migratory locust).							
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;							
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caenifera;							
OC Acridermorpha; Acridoidea; Acridae; Oedipodinae; Locusta.							
NCBI_TAXID=7004;							
RN [1]							
RP SEQUENCE.							
RC TISSUE="Corpora cardiaca";							
RX MEDLINE=93262881;							
RA Schoofs L., Holman G.M., Proost P., van Damme J., Hayes T.K.,							
RT de Looff A.,							
"Locustakinin, a novel myotropin peptide from <i>Locusta migratoria</i> , isolation, primary structure and synthesis.";							
RL Regul. Pept. 37:49-57(1992).							
CC -1- FUNCTION: MYOTROPIC PEPTIDE. MAY BE IMPORTANT IN THE STIMULATION OF ION TRANSPORT AND INHIBITION OF DIURETIC ACTIVITY IN MALPIGHIAN TUBULES.							
DR PIR: A61068; A61068.							
KW Neuropeptide; Amidation.							
FT MOD_RES							
SQ SEQUENCE 6 AA; 654 MW; 686365A5B9CDB000 CRC64;							
Query Match	24.7%	Score 22;	DB 1;	Length 6;			
Best Local Similarity	75.0%	Pred. No. 1.1e+05;					
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;							
Qy 2 NSWG 5							
Db 3 SSWG 6							
RESULT 11							
LCK2_LEUMA	STANDARD;	PRT;	8 AA.				
ID P2141;							
DT 01-MAY-1991 (Rel. 18, Created)							
DT 01-MAY-1991 (Rel. 18, Last sequence update)							
DE 01-MAY-1991 (Rel. 18, Last annotation update)							
OS Leucokinin II (L-II).							
OC Leucophila madeirensis (Madeira cockroach).							
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;							
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;							
OC Blaberidae; Blaberidae; Leucophila.							
NCBI_TAXID=6988;							
RP SEQUENCE, AND SYNTHESIS.							
RC TISSUE=Head;							
RA Holman G.M., Cook B.J., Nachman R.J.;							
RT "Isolation, primary structure and synthesis of two neuropeptides from Leucophila madeirensis: members of a new family of Comp. Biochem. Physiol. 84C:205-211(1986).							
CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE ACTIVITY OF COCKROACH PROTEODEUM (HINDGUT).							
KW -1- SIMILARITY: TO THE OTHER LEUCOKININS.							
FT MOD_RES							
SQ SEQUENCE 8 AA; 905 MW; DC6365B1E955BDDA CRC64;							
Query Match	24.7%	Score 22;	DB 1;	Length 8;			
Best Local Similarity	75.0%	Pred. No. 1.1e+05;					
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;							
Qy 2 NSWG 5							
Db 3 SSWG 6							
RESULT 12							
LCK4_LEUMA	STANDARD;	PRT;	8 AA.				
ID LCK4_LEUMA							
AC P21143;							
DT 01-MAY-1991 (Rel. 18, Created)							
DT 01-MAY-1991 (Rel. 18, Last sequence update)							
DE 01-MAY-1991 (Rel. 18, Last annotation update)							
RA Leucokinin IV (L-IV).							
RC Leucophila madeirensis (Madeira cockroach).							
CC Insecta; Pterygota; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;							
CC Blaberidae; Blaberidae; Leucophila.							
NCBI_TAXID=6988;							
RP SEQUENCE.							
RC TISSUE=Head;							
RA Holman G.M., Cook B.T., Nachman R.J.;							
RT "Isolation, primary structure, and synthesis of leucokinins V and VI: myotrophic peptides of Leucophila madeirensis.";							
CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE ACTIVITY OF COCKROACH PROTEODEUM (HINDGUT).							
KW -1- SIMILARITY: TO THE OTHER LEUCOKININS.							

DR PIR; JS0315; JS0315;
 KW Neuropeptide; Amidation.
 FT MOD-RES 8 AMIDATION;
 SQ SEQUENCE 8 AA; 784 MW; 736365A5B9C65B8 CRC64;

Query Match 24.7%; Score 22; DB 1; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1.1e+05; 1; Mismatches 0; Indels 0; Gaps 0;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 NSWG 5 :111
 Db 5 SSWG 8

RESULT 14
 LCK6_LEMMA STANDARD; PRT; 8 AA.
 ID LCK6_LEMMA
 AC P19988;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Leucokinin VI (L-VI).
 OS Leucophaea maderae (Madeira cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Blattaria;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blaberidae; Leucophaeidae.
 OC NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE.
 RT TISSUE="head";
 RX MEDLINE=8705651; PubMed=2877794;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT "Isolation, primary structure, and synthesis of leucokinins V and VI: myotropic peptides of Leucophaeidae madeae.";
 RL Comp. Biochem. Physiol. 88C:27-30 (1987).
 CC -1- FUNCTION: THIS CEPHALOMYTROPIIC PEPTIDE STIMULATES CONTRACTILE ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
 CC -1- SIMILARITY: TO THE OTHER LEUCOKININS, AND TO MANDUCA SEXTA AND HELIOMIHS ZEA ADIPOKINETIC HORMONE.
 CC PIR: JS0316; JS0316.
 KW Neuropeptide; Amidation.
 FT MOD-RES 1 1 AMIDATION;
 SQ SEQUENCE 8 AA; 935 MW; 9b6365B1E9D5A5A6 CRC64;

Query Match 24.7%; Score 22; DB 1; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1.1e+05; 1; Mismatches 0; Indels 0; Gaps 0;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 NSWG 5 :111
 Db 5 HSWG 8

RESULT 15
 LCK7_LEMMA STANDARD; PRT; 8 AA.
 ID LCK7_LEMMA
 AC P19985;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE Leucokinin VII (L-VII).
 OS Leucophaeidae maderae (Madeira cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Blattaria;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blaberidae; Blaberidae; Leucophaeidae.
 OC NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE.
 RT TISSUE="head";
 RX MEDLINE=8705651; PubMed=2877794;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT "Isolation, primary structure and synthesis of leucokinins VII and VIII: the final members of this new family of cephalomyotrophic

RESULT 16
 CEP1_ACHFU STANDARD; PRT; 11 AA.
 ID CEP1_ACHFU
 AC P22790;
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-AUG-1991 (Rel. 19, Last annotation update)
 DE 01-DEC-1992 (Rel. 24, Last annotation update)
 CC Cephalomyotrophic Peptide-1 (ACEP-1).
 OS Achatina fulica (Giant African snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Styliommatophora; Achatinaceae; Achatinidae; Achatina.
 OC NCBI_TaxID=6530;
 RN [1]
 RP SEQUENCE.
 RT STRAIN="Ferussac"; TISSUE="Heart atrium";
 RX MEDLINE=902161; PubMed=2322251;
 RA Fujimoto K., Ohta N., Yoshida M., Kubota I., Muneoka Y., Kobayashi M.;
 RT "A novel cardio-excitatory peptide isolated from the atria of the African giant snail, Achatina fulica.";
 RL Biochem. Biophys. Res. Commun. 167:777-783 (1990).
 CC -1- FUNCTION: POTENTIATES THE BEAT OF THE VENTRICLE, AND HAS ALSO EXCITATORY ACTIONS ON THE PENTS RETRACTOR MUSCLE, THE Buccal Muscle AND THE IDENTIFIED NEURONS CONTROLLING THE Buccal Muscle.
 CC -1- SIMILARITY: TO POSSIBLE PEPTIDE LS FROM APLYSIA.
 DR PIR: A34662; A34662.
 KW Hormone; Amidation.
 FT MOD-RES 11 11 AMIDATION;
 SQ SEQUENCE 11 AA; 1305 MW; 82D6D5B9C7/41365 CRC64;

Query Match 24.7%; Score 22; DB 1; Length 11;
 Best Local Similarity 57.1%; Pred. No. 8.4e+02; 1; Mismatches 2; Indels 0; Gaps 0;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 SSWGKR 9 :111
 Db 4 SWRPFQGR 10

RESULT 17
 LCK_DROME STANDARD; PRT; 15 AA.
 ID LCK_DROME
 AC P81029;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Leucokinin (Dk).
 GN PP OR DIK.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Bphydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]

RP SEQUENCE:
 RC TISSUE=Seed;
 RX MEDLINE=89206218; PubMed=2705782;
 RA Young N.M.; Johnston R.A.Z.; Szabo A.G.; Watson D.C.;
 RT "Homology of the D-galactose-specific lectins from *Artocarpus integrifolia* and *Macfura pomifera* and the role of an unusual small polypeptide subunit.";
 RL Arch. Biochem. Biophys. 270:596-603(1989).
 RN [2]
 RP SEQUENCE:
 RX MEDLINE=92287028; PubMed=1590914;
 RA Mahanta S.K.; Sanker S.; Prasad Rao N.V.S.A.V.; Swamy M.J.;
 RA Surolia A.;
 RT *Artocarpus integrifolia* (Jack fruit) agglutinin. Evidence for the presence of an internal repeat.;
 RL Biochem. J. 284:95-101(1992).
 CC -1- FUNCTION: D-GALACTOSE-SPECIFIC LECTIN, BINDS THE T-ANTIGEN-STRUCTURE GAL-3-GALNAc (THOMSEN-FRIEDEMREICH-ANTIGEN-SPECIFIC LECTIN).
 CC -1- FUNCTION: POTENT AND SELECTIVE STIMULANT OF DISTINCT T- AND B-CELL FUNCTIONS. SHOWS A UNIQUE ABILITY TO SPECIFICALLY RECOGNIZE IGA-1 FROM HUMAN SERUM.
 CC -1- SUBUNIT: TETRAMER OF FOUR ALPHA CHAIN ASSOCIATED WITH TWO OR FOUR BETA CHAINS.
 CC -1- SIMILARITY: TO THE OTHER AGGLUTININ BETA CHAINS.
 DR PIR; 503985; S03985.
 Lectin; IGA-binding protein. 894AFC9899B0E212 CRC64;
 SQ SEQUENCE 20 AA; 2058 MW; 894AFC9899B0E212 CRC64;
 Query Match 24.7%; Score 22; DB 1; Length 20;
 Best Local Similarity 75.0%; Pred. No. 1.4e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 4 WGCK 7
 Db 15 WGAK 18

RESULT 21
 LCK8-LEUMA STANDARD: PRT; 8 AA.
 AC P19990;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DE Leucokinin VIII (L-VIII).
 OS Leucophaeia maderae (Madeira cockroach).
 OC Eukaryota: Metazoa; Arthropoda; Mandibulata; Pauciraspae; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blaberoidea; Blaberidae; Leucophaeia.
 OX NCBI_TaxID=6988;
 RN [1]
 SEQUENCE.
 RC TISSUE=Head;
 RA Holman G.M.; Cook B.J.; Nachman R.J.;
 RT Isolation, primary structure and synthesis of leucokinins VII and VIII: the final members of this new family of cephalomyotoxic peptides isolated from head extracts of *Leucophaeia maderae*.;
 RT -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE ACTIVITY OF COCKROACH PROTOPODEUM (HINDGUT).
 RL Comp. Biochem. Physiol. 88C:31-34(1987).
 CC PIR; JS0318; JS0318.
 DR Neuropeptide; Amidation.
 FT MOD_RES 8 AMIDATION.
 SQ SEQUENCE 8 AA; 902 MW; 736365Ab5CADD8 CRC64;
 Query Match 23.6%; Score 21; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 3 SWG 5

Db 6 SWG 8
 RESULT 22
 ID TACI-TACG
 ID TACI-TACG1 STANDARD: PRT; 17 AA.
 AC P23684;
 DT 01-NOV-1991 (Rel. 20, created)
 DT 01-Nov-1991 (Rel. 20, last sequence update)
 DE Tachyplesin I (Rel. 32, last annotation update)
 OS Tachyplesin I (Rel. 32, last annotation update)
 OS Tachyplesius gigas (Southeast Asian horseshoe crab), and *Carcinoscorpius rotundicauda* (Southeast Asian horseshoe crab).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura; Limulidae; Tachyplesius.
 OC NCBI_TaxID=6852; 6848;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=T. gigas, and *C. rotundicauda*;
 RX MEDLINE=9103537; PubMed=2222025;
 RA Muta T.; Fujimoto T.; Nakajima H.; Iwanaga S.;
 RT "Tachyplesins isolated from hemocytes of Southeast Asian horseshoe crabs (*Carcinoscorpius rotundicauda* and *Tachyplesius gigas*): identification of a new tachyplesin, tachyplesin III, and a processing intermediate of its precursor.";
 RT Biochem. 108:261-266(1990).
 CC -1- SIMILARITY: BELONGS TO THE TACHYPLESIN/POLYPHEMUSIN FAMILY.
 DR PIR; A3824; A3824;
 DR PIR; A3824; A3824;
 DR PIR; JX0124; JX0124;
 KW Antibiotic; Amidation.
 FT DISULFID 3 16
 FT DISULFID 7 12
 FT MOD_RES 17 17 AMIDATION.
 SQ SEQUENCE 17 AA; 2269 MW; E9E09BD923C94 CRC64;
 Query Match 23.6%; Score 21; DB 1; Length 17;
 Best Local Similarity 80.0%; Pred. No. 1.8e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 9 RICCY 13
 Db 9 RGICY 13

RESULT 23
 ID TAC3-TACG1 STANDARD: PRT; 17 AA.
 AC P18252;
 DT 01-Nov-1990 (Rel. 16, Created)
 DT 01-Nov-1990 (Rel. 16, Last sequence update)
 DT 01-Nov-1990 (Rel. 32, Last annotation update)
 DE Tachyplesin III.
 OS Tachyplesius gigas (Southeast Asian horseshoe crab).
 OC Eukaryota; Metazoa; Chelicerata; Merostomata; Xiphosura; Limulidae; Tachyplesius.
 OX NCBI_TaxID=6852;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=9103537; PubMed=2222025;
 RA Muta T.; Fujimoto T.; Nakajima H.; Iwanaga S.;
 RT "Tachyplesins isolated from hemocytes of Southeast Asian horseshoe crabs (*Carcinoscorpius rotundicauda* and *Tachyplesius gigas*): identification of a new tachyplesin, tachyplesin III, and a processing intermediate of its precursor.";
 RT Biochem. 108:261-266(1990).
 RL J. Biochem. 108:261-266(1990).
 CC -1- TISSUE SPECIFICITY: HEMOCYTES.
 CC -1- SIMILARITY: BELONGS TO THE TACHYPLESIN/POLYPHEMUSIN FAMILY.
 DR PIR; JX0125; JX0125;
 KW Antibiotic; Amidation.
 FT DISULFID 3 16 BY SIMILARITY.

PT DISULFID 7 12 BY SIMILARITY.
 FT MOD_RES 17 17 AMIDATION.
 SQ SEQUENCE 17 AA; 2241 MW; E9E08CE9D2923C94 CRC64;

Query Match 23.6%; Score 21; DB 1; Length 17;
 Best Local Similarity 80.0%; Pred. No. 1.8e+03; Mismatches 1; Indels 0; Gaps 0;

OY 9 RICY 13
 Db 9 RGICY 13

RESULT 24

CXLI_CONMR STANDARD; PRT; 11 AA.

AC P58807; DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Lambda-conotoxin CMV1A.
 OS Conus marmoreus (Marble cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TAXID=42752;
 RN [1]
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
 RC TISSUE="Venom";
 RX MEDLINE=20564325; PubMed=10980292;
 RA Balaji R.A., Onitsuka A., Sato K., Gopalakrishnakone P., Kini R.M.,
 Seow K.T., Bay B.H.,
 "Lambda-conotoxins, a new family of conotoxins with unique disulfide pattern and protein folding. Isolation and characterization from the venom of Conus marmoreus.",
 J. Biol. Chem. 275:39516-39522(2000).
 J. Biol. Chem. 275:39516-39522(2000).
 -i- FUNCTION: Inhibits the neuronal noradrenaline transporter.
 -i- SUBCELLULAR LOCATION: Secreted.
 -i- TISSUE SPECIFICITY: Expressed by the venom duct.
 -i- MASS SPECTROMETRY: MW=127.93; MW_ERR=0.21; METHOD=Electrospray.
 CC BELONGS TO THE CHI/LAMBDA-CONOTOXIN FAMILY.
 KW Neurotoxin; Toxin; Hydroxylation.
 FT DISULFID 2 11
 FT DISULFID 3 8
 PT MOD_RES 10 10 HYDROXYLATION.
 SQ SEQUENCE 11 AA; 1226 MW; 277AAC60B723B58 CRC64;

Query Match 22.5%; Score 20; DB 1; Length 11;
 Best Local Similarity 37.5%; Pred. No. 1.8e+03; Mismatches 3; Indels 0; Gaps 0;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 6 CKGRICY 13
 Db 2 CCGYKLCH 9

RESULT 25

TIN3_HOPTR STANDARD; PRT; 12 AA.

AC P82653; DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 TIGERININ-3.
 OC Hoplobatrachus tigerinus (Indian bull frog) (*Rana tigerina*).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae;
 OC Hoplobatrachus.
 OX NCBI_TAXID=10373;
 [1]
 RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
 RC TISSUE="Skin";
 RX PubMed=11031261;
 RA Purva Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,

RA Devi A.S., Nagaraj R., Sitaram N.;
 RT "Nigerinins": novel antimicrobial peptides from the Indian frog *Rana tigrina*.;
 RT J. Biol. Chem. 276:2701-2707/2001).
 CC -i- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST *B.SUBTILIS*, *E.COLI*, *S.AUREUS*, *M.LUTUS*, *P.PUTIDA* AND *S.CEREVISIAE*.
 CC -i- SUBCELLULAR LOCATION: Secreted.
 CC -i- TISSUE SPECIFICITY: SKIN.
 CC -i- MASS SPECTROMETRY: MW=1109; METHOD=MALDI.
 KW Amphibian skin; Antibiotic; Amidation.

RESULT 26

CXLI_CONMR STANDARD; PRT; 13 AA.

AC P58810; DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Lambda/chi-conotoxin Mr1B (Chi-Mr1B).
 OS Conus marmoreus (Marble cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OX NCBI_TAXID=42752;
 RN [1]
 RP SEQUENCE, SYNTHESIS, AND STRUCTURE BY NMR.
 RC TISSUE="Venom";
 RX MEDLINE=21419681; PubMed=11528421;
 RA Sharpe T.A., Gehrmann J., Loughnan M.L., Thomas L., Adams D.A.,
 RA Atkins A., Palant E., Craik D.J., Adams D.J., Alewood P.F.,
 RA Lewis R.J.;
 "Two new classes of conopeptides inhibit the alpha1-adrenoceptor and
 RT noradrenaline transporter.";
 RL Nat. Neurosci. 4:902-907/2001).
 CC -i- FUNCTION: Inhibits the neuronal noradrenaline transporter.
 CC -i- SUBCELLULAR LOCATION: Secreted.
 CC -i- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -i- PTM: Exists in two forms, due to cis-trans isomerization at His-
 CC 11-Hyp-1.
 CC -i- MASS SPECTROMETRY: MW=1393.52; METHOD=Electrospray.
 DR PDB: 1IEO; 03-APR-02.
 KW Neurotoxin; Toxin; Hydroxylation; 3D-structure.

FT DISULFID 4 13
 FT DISULFID 5 10 HYDROXYLATION.
 FT MOD_RES 12 12 HYDROXYLATION.
 SQ SEQUENCE 13 AA; 1382 MW; 277AAC376EAD2B58 CRC64;

Query Match 22.5%; Score 20; DB 1; Length 13;
 Best Local Similarity 37.5%; Pred. No. 2e+03; Mismatches 3; Indels 0; Gaps 0;

OY 6 CKGRICY 13
 Db 4 CCGYKLCH 11

RESULT 27

SMS1_MYO5C STANDARD; PRT; 14 AA.

AC P20750; DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, last sequence update)
 DT 16-OCT-2001 (Rel. 40, last annotation update)
 DE Somatostatin I.
 OS Myoxocephalus scorpius (Shorthorn sculpin) (Daddy sculpin), and
 OS Oncopterus dumerilii (European freshwater eel);
 OS Anguilla anguilla (European freshwater eel);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Scorpaeniformes;
 OC Cottidae; Cottidae; Myoxocephalus.
 OX NCBI_TAXID=8097, 8019, 7936;
 RN [1]
 RP SEQUENCE.
 RC SPECIES="M. scorpis"; TISSUE="Pancreas";
 RX MEDLINE=88029436; PubMed=2880597;
 RA Conlon J.M., Davis M.S., Falkner S., Thim L.;
 RT "Structural characterization of peptides derived from
 pro somatostatins I and II isolated from the pancreatic islets of two
 species of teleostean fish: the daddy sculpin and the flounder.";
 RT Eur. J. Biochem. 168:647-652 (1987).
 RL [2]
 RP SEQUENCE.
 RC SPECIES="O. kisutch"; TISSUE="Pancreas";
 RX MEDLINE=87055212; PubMed=287939;
 RA Plisetskaya E.M., Pollock H.G., Rouse J.B., Hamilton J.W.,
 Kimmel J.R., Andrews P.C., Gorbman A.;
 RT "Characterization of coho salmon (Oncorhynchus kisutch) islet
 somatostatins.";
 RL Gen. Comp. Endocrinol. 63:252-263 (1986).
 RN [3]
 RP SEQUENCE.
 RC SPECIES="A. anguilla"; TISSUE="Pancreas";
 RX MEDLINE=89065329; PubMed=2904391;
 RA Conlon J.M., Deacon C.F., Hazon N., Henderson I.W., Thim L.;
 RT "Somatostatin-related and glucagon-related peptides with unusual
 structural features from the European eel (Anguilla anguilla).";
 RT Gen. Comp. Endocrinol. 72:181-189 (1988).
 CC -!- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.
 DR PIR: S00172; S00122.
 DR B60842;
 PIR: A60840; A60840;
 DR InterPro; IPR04250; Somatostatin.
 DR Pfam; PF03002; Somatostatin_1.
 KW Hormone; Multigene family.
 FT DISULFID 3 14 AA; 1640 MW; D6270F5C09682679 CRC64;
 SQ SEQUENCE 14 AA; 1640 MW; BY SIMILARITY.
 OY 3 14 AA; 1640 MW; D6270F5C09682679 CRC64;
 DB 2 GCK 4

RESULT 29
 CX1B_CONBE
 ID CX1B_CONBE
 AC P58624;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Conotoxin BerXIB.
 OS Conus betulinus (Beech cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TAXID=89764;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE="Venom";
 RX MEDLINE=20058566; PubMed=10591037;
 RA Chen J.-S., Fan C.-X., Hu K.-P., Wei K.-H., Zhong M.-N.;
 RT "Studies on conotoxins of Conus betulinus.";
 RL J. Nat. Toxins 8:341-349 (1999).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- MASS SPECTROMETRY: MW=1642.5; METHOD=MALDI.
 CC -!- SIMILARITY: BELONGS TO THE M-SUPERFAMILY OF CONOTOXINS.
 KW Neurotoxin; Toxin.
 FT PROBABLE.
 FT DISULFID 1 9 PROBABLE.
 FT DISULFID 2 12 PROBABLE.
 FT DISULFID 6 13 PROBABLE.
 SQ SEQUENCE 15 AA; 1650 MW; 3749B4F08E31137 CRC64;
 OY 6 CKGRIC 12
 DB 6 CHGCYPC 12

RESULT 28
 SNS_ALMMI STANDARD; PRT; 14 AA.
 ID SNS_ALMMI
 AC P31855;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Somatostatin-14.
 OS Alligator mississippiensis (American alligator), and
 OS Trachemys scripta (Red-eared slider turtle) (Pseudemys scripta).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Archosauvia; Crocodylia; Alligatorinae; Alligator.
 OX NCBI_TAXID=8496, 34903;
 RN [1]
 RP SEQUENCE.

RESULT 30
 ISOT_CYPCA

ID ISOT_CIPCA STANDARD; PRT; 9 AA.
 AC P4293; PRT;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE Isotocin.
 OS Cyprinus carpio (Common carp).
 BU Karvヨta; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Cyprinus.
 OX NCBI_TaxID:7962;
 RN [1]
 RP
 RC
 SEQUENCE.
 TISSUE=pituitary;
 RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
 RT "Characterization of neurohypophyseal hormones from a fresh water bony
 fish, the carp (Cyprinus carpio). Comparison with hormones from sea
 water bony fishes."
 RL Comp. Biochem. Physiol. 14:245-254 (1965).
 CC -1- FUNCTION: ANTIDIURETIC HORMONE.
 DR -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 PIR: A61364; A61364.
 InterPro: IPR000981; Neurhyp-horm.
 DR InterPro: IPR001230; Prenyl-site.
 DR Pfam: PF00220; hormone_1.
 DR Hormone; Amidation.
 KW Hormone; Amidation.
 FT DISULFID 1 6
 FT MOD_RES 9 9 AMIDATION.
 FT SEQUENCE 9 AA; 969 MW; 17FF476EB455B04B CRFC64;
 Query Match 21.3%; Score 19; DB 1; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1.1e-05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 12 CYS 15
 Db 1 CYS 4

Search completed: June 5, 2003, 08:59:40
 Job time : 13 secs

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Om protein - protein search, using sw model

Run on:

June 5, 2003, 08:58:43 ; Search time 27 Seconds

(without alignments)

114.471 Million cell updates/sec

Title: US-09-605-573a-69_COPY_12_26

Perfect score: 89

Sequence: 1 LNSWGCKGRICGTC 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters:

6395

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

SPREMBL-21,*

1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriop:*

17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

1	27	30.3	8	5	P82685	P82685 periplaneta	Q45663 bacillus su
2	27	30.3	8	5	P82687	P82687 periplaneta	Q96c65 homo sapien
3	27	30.3	8	5	P82689	P82689 periplaneta	P82688 periplaneta
4	27	30.3	17	6	Q9nQ25	Q9tqz5 macaca fasc	P82688 periplaneta
5	27	30.3	20	10	Q9s8T1	Q9s8T1 arccarpus	Q56947 yersinia ps
6	25	28.1	15	12	Q86543	Q86543 human herpe	Q93794 streptococc
7	25	28.1	15	12	Q86576	Q86576 subterranea	Q9x112 hemisila tab
8	24.5	27.5	20	13	Q9DE23	Q9s823 gallus gall	Q9s311 rhodospiril
9	24	27.0	12	15	Q12036	Q12036 caprine art	Q85004 porcine res
10	24	27.0	17	17	Q06800	Q06800 saccharomy	Q9qvl0 mus sp. mep
11	24	27.0	20	10	Q9XiW8	Q9XiW8 orza sativ	Q9prf0 oryzas lat
12	24	27.0	20	10	Q9s8E0	Q9s8E0 apium grave	Q8v157 mus musculi
13	24	27.0	20	11	Q9QK8	Q9QK8 rattus sp.	Q93two neisseria m
14	24	27.0	20	12	Q84861	Q84861 unidentifie	Q66202 transmissib
15	23	25.8	10	2	Q5032	Q5032 mycobacteri	P83077 bacillus ce
16	23	25.8	12	7	Q31006	Q31006 bos taurinus	Q9t899 oreochromis
17							Q9trp3 hordeum vul
18							Q9p229 bos taurus
19							Q8w118 oreochromis
20							Q8w120 oreochromis
21							Q8w64 anolis lunc
22							Q8w833 anolis nite
23							Q8w899 oreochromis
24							Q8w900 oreochromis
25							Q77891 oreochromis
26							Q77892 pseudochromis
27							Q78118 pseudochromis
28							Q78120 oreochromis
29							Q96f82 chelosenia
30							Q96f83 chelosenia
31							Q9trp3 scyllorhinu
32							Q9trp4 petromyzon
33							Q9trp5 zebrafish
34							Q9trp6 hordeum vul
35							Q9trp7 pyrococcus
36							Q9trp8 salmonella
37							Q9trp9 mus musculu
38							Q9trp10 neisseria
39							Q9trp11 salmonella
40							Q9trp12 pseudomonas
41							Q9trp13 pseudomonas
42							Q9trp14 pseudomonas
43							Q9trp15 pseudomonas
44							Q9trp16 pseudomonas
45							Q9trp17 pseudomonas
46							Q9trp18 pseudomonas
47							Q9trp19 pseudomonas
48							Q9trp20 pseudomonas
49							Q9trp21 pseudomonas
50							Q9trp22 pseudomonas
51							Q9trp23 pseudomonas
52							Q9trp24 pseudomonas
53							Q9trp25 pseudomonas
54							Q9trp26 pseudomonas
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56							Q9trp28 pseudomonas
57							Q9trp29 pseudomonas
58							Q9trp30 pseudomonas
59							Q9trp31 pseudomonas
60							Q9trp32 pseudomonas
61							Q9trp33 pseudomonas
62							Q9trp34 pseudomonas
63							Q9trp35 pseudomonas
64							Q9trp36 pseudomonas
65							Q9trp37 pseudomonas
66							Q9trp38 pseudomonas
67							Q9trp39 pseudomonas
68							Q9trp40 pseudomonas
69							Q9trp41 pseudomonas
70							Q9trp42 pseudomonas
71							Q9trp43 pseudomonas
72							Q9trp44 pseudomonas
73							Q9trp45 pseudomonas
74							Q9trp46 pseudomonas
75							Q9trp47 pseudomonas
76							Q9trp48 pseudomonas
77							Q9trp49 pseudomonas
78							Q9trp50 pseudomonas
79							Q9trp51 pseudomonas
80							Q9trp52 pseudomonas
81							Q9trp53 pseudomonas
82							Q9trp54 pseudomonas
83							Q9trp55 pseudomonas
84							Q9trp56 pseudomonas
85							Q9trp57 pseudomonas
86							Q9trp58 pseudomonas
87							Q9trp59 pseudomonas
88							Q9trp60 pseudomonas
89							Q9trp61 pseudomonas

RA NICOLAS M.G.; Fujiki K.; Murayama K.; Suzuki M.T.; Mineki R.; RA Hayakawa M.; Yoshihikawa Y.; Cho F.; Kanai A.; "Studies on the mechanism of early onset macular degeneration in RT cynomolgus (Macaca fascicularis) monkeys. I. Abnormal concentrations of two proteins in the retina."; Exp. Eye Res. 62:211-219(1996); RL EXP. Eye Res. 62:211-219(1996);

-1- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE + PHOSPHATE + NAD(+)= 3-PHOSPHO-D-GLYCEROYL PHOSPHATE + NADH.

-1- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE FAMILY.

DR InterPro: IPR00173; GAP_dihydrogenase.

DR Pfam: PF00044; gpdh; 1.

KW GLYCOLYSIS; NAD; Oxidoreductase.

SQ SEQUENCE 17 AA; 1671 MW; 52CCD01A98B3DAF CRC64;

Query Match 30.3%; Score 27; DB 6; Length 17; Best Local Similarity 36.4%; Pred. No. 6.4e+02; Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LNSWGCKGRII 11

Db 7 VNGFGAIGRLV 17

RESULT 5

Q9S8T1 PRELIMINARY; PRT; 20 AA.

ID Q9S8T1; PRELIMINARY; PRT; 20 AA.

AC 09S8T1; PRELIMINARY; PRT; 20 AA.

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Jacalin beta-subunit (Fragment).

OS Artocarpus tonkinensis.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; eudicots; rosidae; euRosids I; Rosales; Moraceae; Artocarpus.

OX NCBI_TaxID=3492;

RN [1]

RP SEQUENCE.

RX MEDLINE=91152601; PubMed=8427879;

RA NGOC L.D.; Brillard M.; Hoebeke J.; "The alpha- and beta-subunits of the Jacalins are cleavage products from a 17-kDa precursor"; RY Biocim. Biophys. Acta 1156:219-222(1993).

FT NON-TER 1

FT NON-TER 20

SQ SEQUENCE 20 AA; 2131 MW; 89489367060EFFE CRC64;

Query Match 30.3%; Score 27; DB 10; Length 20; Best Local Similarity 57.1%; Pred. No. 7.6e+02; Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LNSWGCK 7

Db 12 VGSNGAK 18

RESULT 6

Q9D543 PRELIMINARY; PRT; 15 AA.

ID Q9D543; PRELIMINARY; PRT; 15 AA.

AC 065543; PRELIMINARY; PRT; 15 AA.

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 14, Last annotation update)

DE Epitope C11 (16 AA) (Fragment)

OS Human herpesvirus 4 (Epstein-Barr virus).

OC Virus; dsDNA viruses, no RNA stage; Herpesviridae; Gammapapovirus; Lymphocryptovirus.

OX NCBI_TaxID=10376;

[1]

RP SEQUENCE FROM N.A.

RC STRAIN=B95-8;

RX MEDLINE=8829642; PubMed=2841116;

RA Walls D.; Gannon F.; RT "The expression of novel antigens from the Epstein-Barr virus large internal repeat"; RT RY EMBO J. 7:1191-1196(1988).

RL DR EMBL: X07814; CAA30673.1; -.

FT NON_TER 1 1 15 15

FT NON_TER 15 15

SQ SEQUENCE 15 AA; 1629 MW; 48BA5A4558C3266C CRC64;

Query Match 28.1%; Score 25; DB 12; Length 15; Best Local Similarity 66.7%; Pred. No. 1.2e+03; Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 WGCKGR 9

Db 6 WGKSR 11

RESULT 7

Q86576 PRELIMINARY; PRM; 15 AA.

ID Q86576 PRELIMINARY; PRM; 15 AA.

AC Q86576; PRELIMINARY; PRM; 15 AA.

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE Coat protein (Fragment).

GN Coat PROTEIN.

OS Subterranean clover stunt virus.

OC Viruses; ssDNA viruses; Nanovirus.

OX NCBI_TaxID=6772;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=93212590; PubMed=8460528;

RA Chu P.W.; Keese P.; Qu B.S.; Waterhouse P.M.; Gerlach W.L.; "Putative full-length clones of the genomic DNA segments of subterranean clover stunt virus and identification of the segment coding for the viral coat protein"; RY Virus Res. 27:161-17(1993).

FT DR EMBL; S57687; AAB25908; 1; -.

SQ SEQUENCE 15 AA; 1825 MW; 44D9C8497CD96FFD CRC64;

Query Match 28.1%; Score 25; DB 12; Length 15; Best Local Similarity 80.0%; Pred. No. 1.2e+03; Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 WGCKG 8

Db 5 WGRKG 9

RESULT 8

Q9DE23 PRELIMINARY; PRT; 20 AA.

ID Q9DE23 PRELIMINARY; PRT; 20 AA.

AC Q9DE23; PRELIMINARY; PRT; 20 AA.

DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE UORF2.

OS Gallus gallus (Chicken).

OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus gallus (Chicken).

OX NCBI_TaxID=9031;

[1]

RP SEQUENCE FROM N.A.

RX MEDLINE=0528016; PubMed=11073974;

RA Kobayashi M.; Yu R.T.; Yasuda K.; Umesono K.; "Cell-type-specific regulation of the retinoic acid receptor mediated by the orphan nuclear receptor RXR"; RY Mol. Cell. Biol. 20:8731-8739(2000).

DR EMBL: AR20160; AMG3563.1; -.

DR InterPro: IPR000345; CycC_heme_bind.

DR	InterPro; IPR003006; Ig-MHC.
DR	PS00190; CYTOCHROME_C; UNKNOWN_1.
DR	PROSITE; PS00290; Ig-MHC; UNKNOWN_1.
SQ	SEQUENCE 20 AA; 2261 MW; AA7738B0B3C482 CRC64;
QY	1 LNSWGCKGRRCIYTS 15.
QY	27.5%; Score 24.5; DB 13; Length 20; Best Local Similarity 26.7%; Pred. No. 2e+03; Mismatches 4; Conservative 5; Mismatches 3; Indels 3; Gaps 1;
DB	9 LQAFSC--WVCHNS 20
RESULT 9	
QY	1 LNSWGCKGRRCIYTS 15.
ID	012036 PRELIMINARY; PRT; 12 AA.
AC	012036; 01-JUL-1997 (TREMBrel. 04, Created)
DT	01-JUL-1997 (TREMBrel. 04, Last sequence update)
DT	01-DEC-2001 (TREMBrel. 19, Last annotation update)
DE	Envelope glycoprotein (Fragment).
GN	
OS	Caprine arthritis encephalitis virus (CAEV).
OC	Viruses; Retroviridae; Lentivirus.
OX	NCBI_TAXID=11660;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=97295261; Pubmed=9151845; Turelli, P.; Guiguen, F.; Vigne, R.; Querat, G.; "dimpase-minus" caprine arthritis-encephalitis virus is attenuated for pathogenesis and accumulates G-to-A substitutions.%; J. Virol. 71:4522-4530(1997).
DR	EMBL; U81390; AAC57905; 1; -.
FT	NON_TER 1 1
SQ	SEQUENCE 12 AA; 1398 MW; 8D24228CA3733455 CRC64;
QY	2 NSWGC 6
QY	27.0%; Score 24; DB 15; Length 12; Best Local Similarity 50.0%; Pred. No. 1.5e+03; Mismatches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
DB	6 NKWTC 10
RESULT 10	
QY	1 LNSWGCKGRRCIYTS 15.
ID	006800 PRELIMINARY; PRT; 17 AA.
AC	006800; 01-NOV-1996 (TREMBrel. 01, Created)
DT	01-NOV-1996 (TREMBrel. 01, Last sequence update)
DT	01-JUN-2002 (TREMBrel. 21, Last annotation update)
DE	N1780.
GN	LSM7 OR N1780 OR YNL147W.
OS	Saccharomyces cerevisiae (Baker's yeast).
OC	Eukaryota; Fungi; Ascomycota; Saccharomycetes;
OC	Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TAXID=4932;	
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=96287653; Pubmed=8686380;
RA	Nasr, A.M.; Herbert, C.J.;
RT	"the sequence of 36.8 kb from the left arm of chromosome XIV reveals 24 complete open reading frames: 18 correspond to new genes, one of which encodes a protein similar to the human myotonic dystrophy kinase.%; RY, yeast 12:169-175(1996)."
RL	X92517; CAA63282; 1; -.
DR	EMBL; S0005091; LSN7.
SQ	SEQUENCE 17 AA; 2139 MW; BD7E9AAFADE754AF CRC64;
QY	2 NSWGC 5
QY	27.0%; Score 24; DB 3; Length 17; Best Local Similarity 75.0%; Pred. No. 2.4e+03; Mismatches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
DB	16 NNNWG 19
RESULT 13	

Q9QKB	Q9QKB	PRELIMINARY;	PRT;	20 AA.	OS	Mycobacterium leprae.
ID	Q9QKB				OC	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
AC					OC	Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
DT	01-MAY-2000	(TREMBREL. 13, Created)			OX	
DT	01-DEC-2001	(TREMBREL. 19, Last sequence update)			RN	[1]
DE	Alpha class glutathione S-transferase subunit 1B (EC 2.5.1.18)				RP	SEQUENCE FROM N.A.
DE	(Fragment).				RA	Smith D.R.;
OS	Rattus sp.				RL	Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
OC	Eutherota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				RN	[2]
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				RP	SEQUENCE FROM N.A.
OX	NCBI_TaxID=10118;				RA	Robison K;
RN	[1]				RL	Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
RX	MEDLINE=96036981; PubMed=7485987;				DR	EMBL; U15182; AAA62075.1; -.
RA	Rouimi P.; Debrabauer L.; Tulliez J.;				SO	SEQUENCE FROM N.A.
RT	"Electrospray ionization-mass spectrometry as a tool for characterization of glutathione S-transferase isozymes";				QY	Query Match
RT	Anal. Biochem. 228(3):304-312(1995).				QY	25.8%; Score 23; DB 2; Length 10;
RL	DR				QY	Best Local Similarity 60.0%; Pred. NO. 1.8e+03; Mismatches 3;
DR	HSPB; P08263; 1G0H.				Db	Indels 0; Gaps 0;
SQ	SEQUENCE 20 AA; 2421 MW; 949F405B7DA0B236 CRC64;				QY	6 CKGR1 10
Query Match	27.0%; Score 24; DB 11; Length 20;				Db	6 CEGRL 10
Best Local Similarity 33.3%; Pred. NO. 2.4e+03; Mismatches 4; Conservative 4; Indels 4; Gaps 0; Gaps 0;						
RESULT 14					RESULT 16	
Q94861					Q31006	
ID	Q94861	PRELIMINARY;	PRT;	20 AA.	ID	
AC	Q94861;				AC	
DT	01-NOV-1996	(TREMBREL. 01, Created)			DT	
DT	01-NOV-1996	(TREMBREL. 01, Last sequence update)			DT	
DE	01-DEC-2001	(TREMBREL. 19, Last annotation update)			DT	
OS	Hypothetical 2.2 kDa protein (Fragment).				DE	
OC	Unidentified human poliovirus.				GN	
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;				OS	
OC	Enterovirus.				OS	
OX	NCBI_TaxID=40278;				OS	
RN	[1]				OS	
RP	SEQUENCE FROM N.A.				OS	
RX	MEDLINE=87169734; PubMed=3031313;				OS	
RA	Kuge S., Saito T., Nomoto A.;				OS	
RT	"Primary structure of poliovirus defective-interfering particle genomes and possible generation mechanisms of the particles.,"				OS	
RT	J. Mol. Biol. 192:473-487(1986).				OS	
RL	EMBL; M3018; AAA60827.1; -.				OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RW	Hypothetical protein.				OC	Bivalvia; Bivalvia; Bos.
FT	NON_TER 1				OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
FT	NON_TER 20				OC	NCBI_TaxID=9913;
FT	NON_TER 20				RN	[1]
SQ	SEQUENCE 20 AA; 2241 MW; 55D177D10BAF0FF9 CRC64;				RP	SEQUENCE FROM N.A.
Query Match	27.0%; Score 24; DB 12; Length 20;				RX	MEDLINE=93052564; PubMed=1428011;
Best Local Similarity 75.0%; Pred. NO. 2.4e+03; Mismatches 1; Conservative 1; Indels 0; Gaps 0;					RA	Ellis S.A., Braem K.A., Morrison W.I.;
Matches 3; Conservati					RT	"Transmembrane and cytoplasmic domain sequences demonstrate at least two expressed bovine MHC class I loci.,"
QY	2 NSWG 5				RT	RT
Db	7 NWNG 10				RL	Immunogenetics 37:49-56(1992).
RESULT 15					DR	EMBL; S47738; AA23972.1; -.
Q90032					FT	
ID	Q90032	PRELIMINARY;	PRT;	10 AA.	FT	
AC	Q90032;				FT	
DT	01-NOV-1996	(TREMBREL. 01, Created)			FT	
DT	01-NOV-1996	(TREMBREL. 01, Last sequence update)			FT	
DT	01-NOV-1996	(TREMBREL. 01, Last annotation update)			FT	
DE	U22669.				FT	
RX	SEQUENCE FROM N.A.				FT	
RC	STRAIN=MARBURG;				FT	

RX	MEDLINE=85295507; PubMed=293918;	KW	Neuropeptide; Amidation.	
RA	Steinmetz M., Ie Cog D., Aymarich S., Gonzy-Treboul G., Gay P.;	FT	AMIDATION.	
RT	"The DNA sequence of the gene for the secreted <i>Bacillus subtilis</i>	MOD-FES	8	
RT	enzyme levan sucrase and its genetic control sites.";	SEQUENCE	8 AA; 856 MW;	
RL	Mol. Gen. Genet. 200:220-228(1985).	DC6365A5BD5BDAA	CRC64;	
DR	EMBL: X02730; CA26512.1; -;	Query Match	24.7%; Score 22; DB 5; Length 8;	
SQ	SEQUENCE 16 AA; 1840 MW;	Best Local Similarity	75.0%; Pred. No. 6.7e+05;	
Query Match	25.8%; Score 23; DB 2; Length 16;	Matches	1; Mismatches 0; Indels 0; Gaps 0;	
QY	Best Local Similarity 37.5%; Pred. No. 2.9e+03; 3; Mismatches 2; Indels 0; Gaps 0;	QY	2 NSWG 5	
Db	Matches 3; Conservative 3; Conservat 2; Mismatches 1; Indels 0; Gaps 0;	Db	5 SSWG 8	
RESULT 18		RESULT 20		
Q9c65	PRELIMINARY; PRT; 18 AA.	P82688	PRELIMINARY; PRT; 8 AA.	
ID	Q9c65	ID	P82688	
AC	Q9c65;	AC	P82688;	
DT	01-DEC-2001 (TREMBREL. 19, Created)	DT	01-MAR-2001 (TREMBREL. 16, Last sequence update)	
DT	01-DEC-2001 (TREMBREL. 19, Last sequence update)	DT	01-MAR-2001 (TREMBREL. 16, Last annotation update)	
DE	Hypothetical protein.	DE	Kinin-4 (PEA-K-4).	
OS	Homo sapiens (Human).	OS	Periplaneta americana (American cockroach).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea; Blattidae; Periplaneta.	
OX	NCBI_TaxID=9606;	OX	NCBI_TaxID=6978;	
RN	[1] SEQUENCE FROM N.A.	RN	[1] FUNCTION.	
RC	TISSUE=EYE;	RC	SEQUENCE, AND FUNCTION.	
RA	Strausberg R.;	RA	PREDEL R., Kellner R., Rapus J., Penzlin H., Gaede G.;	
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.	RT	Isolation and structural elucidation of eight kinins from the retrocerebral complex of the American cockroach, Periplaneta americana.;	
DR	EMBL: BC014643; ADH14643.1; -;	RT	Regul. Pept. 71:199-205(1997).	
KW	Hypothetical protein. 1	CC	-1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MOTRIPIC ACTIVITY).	
FT	NON_TER 1 18 AA; 2105 MW;	CC	-1- SIMILARITY: BELONGS TO THE KININ FAMILY.	
SEQUENCE	3874A0D25D91AC9C CRC64;	KW	Neuropeptide; Amidation.	
Query Match	25.8%; Score 23; DB 4; Length 18;	FT	AMIDATION.	
Matches	Best Local Similarity 60.0%; Pred. No. 3.2e+03; 2; Mismatches 0; Indels 0; Gaps 0;	SQ	MOD-RES 8	
QY	1 LNSWG 5	Query Match	24.7%; Score 22; DB 5; Length 8;	
Db	1 LDAWG 5	Best Local Similarity 75.0%; Pred. No. 6.7e+05; 1; Mismatches 0; Indels 0; Gaps 0;	QY	2 NSWG 5
RESULT 19		Db	5 SSWG 8	
P82686	PRELIMINARY; PRT; 8 AA.	RESULT 21		
ID	P82686;	Q77914	PRELIMINARY; PRT; 11 AA.	
AC	P82686;	ID	Q77914	
DT	01-MAR-2001 (TREMBREL. 16, Created)	AC	Q77914;	
DT	01-MAR-2001 (TREMBREL. 16, Last sequence update)	DT	01-MAR-1998 (TREMBREL. 08, Last sequence update)	
DE	01-MAR-2001 (TREMBREL. 16, Last annotation update)	DT	01-MAR-2001 (TREMBREL. 19, Last annotation update)	
DE	Kinin-2 (PEA-K-2)	DE	MHC Class II B locus 9 (Fragment).	
OS	Periplaneta americana (American cockroach).	OS	Oreochromis niloticus (Nile tilapia) (Tilapia nilotica)	
OC	Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea; Blattidae; Periplaneta.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygi; Neopterygi; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygi; Perciformes; Labroidei; Ciclidae; Osteochromis.	
OC	NCBI_TaxID=6978;	OC	NCBI_TaxID=8128;	
RN	[1] SEQUENCE, AND FUNCTION.	RN	[1] SEQUENCE FROM N.A.	
RC	TISSUE-CORPORA CARDIACA;	RC	MEDLINE=98315113; PubMed=9649539;	
RX	PREDEL R., Kellner R., Repus J., Penzlin H., Gaede G.;	RA	Malaga-Trillo E., Zalecka Rutczynska Z., McAndrew B., Vincek V.,	
RA	"Isolation and structural elucidation of eight kinins from the retrocerebral complex of the American cockroach, Periplaneta americana.";	RA	Figueroa F., Sultmann H., Klein J.;	
RT	Regul. Pept. 71:199-205(1997).	RT	"Linkage relationships and haplotype polymorphism among cichlid mhc class II B loci.";	
CC	-1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY	RT	Genetics 149:1527-1537(1998).	
CC	(MOTRIPIC ACTIVITY).	RL		
-1- SIMILARITY: BELONGS TO THE KININ FAMILY.				

Query Match 24.7%; Score 22; DB 13; Length 16;
Best Local Similarity 57.1%; Pred. No. 4.3e+03; 0; Mismatches 3; Indels 0; Gaps 0;

Matches 4; Conservative 4; Pred. No. 4e+03; 1; Mismatches 4; Indels 0; Gaps 0;

Qy 6 CKGRICRYCT 14
Db 3 CKPSVTPYT 11

RESULT 26

Q8QVLO PRELIMINARY; PRT; 16 AA.

ID Q8QVLO; PRELIMINARY; PRT; 16 AA.

AC Q8QVLO; PRELIMINARY; PRT; 16 AA.

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE MPRIN-**METALLOENDOPEPTIDASE** (Fragment).

Mus sp.

OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10095;

OX NCBI_TaxID=10095;

RN [1] SEQUENCE.

RX MEDLINE=91363409; PubMed=1888759;

RA Flannery A.V.; Macadam G.C.; Beynon R.J.;"Immunological characterisation of different meprin species in mice."

RT Biochim. Biophys. Acta 1079:119-122(1991).

RL NON-TER 1 1

FT NON-TER 16 16

SQ SEQUENCE 16 AA; 1835 MW; 1409706CRADE119A CRC64;

Query Match Similarity 24.7%; Score 22; DB 11; Length 16; Best Local Similarity 57.1%; Pred. No. 4.3e+03; 1; Mismatches 4; Conservative 4; Matches 4; Conservative 4; Pred. No. 4.3e+03; 2; Indels 0; Gaps 0;

Qy 5 GCKGRIT 11
Db 6 GIKGTVI 12

RESULT 27

Q9PRFO PRELIMINARY; PRT; 16 AA.

ID Q9PRFO; PRELIMINARY; PRT; 16 AA.

AC Q9PRFO; PRELIMINARY; PRT; 16 AA.

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)

DE WNT 5B (Fragment).

GN WNT5/5B.

OS Oryzias latipes (Medaka fish).

OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.

RN [1] NCBI_TaxID=8090;

RP SEQUENCE FROM N.A.

RC STRAIN=RMB;

RX MEDLINE=20082974; PubMed=10613850;

RA Otsuka M., Makino S., Yoda K., Wada H., Naruse K., Mitani H., Shima A., Ozato K., Kimura M., Inoko H.;"Construction of a linkage map of the Medaka (Oryzias latipes) and mapping of the Da mutant (locus defective in dorsoventral patterning). Genome Res. 9:1277-1287(1999)."

RT Genome Res. 9:1277-1287(1999)."

DR EMBL; AB034741; -;

DR EMBL; AB034749; BAA85146.1; -;

FT NON-TER 1 1

SQ SEQUENCE 16 AA; 1802 MW; A7E961E581415DA7 CRC64;

Qy 1 LNSWQCG 6
Db 9 NSWNSLG 15

RESULT 28

Q8V157 PRELIMINARY; PRT; 17 AA.

ID Q8V157; PRELIMINARY; PRT; 17 AA.

AC Q8V157; PRELIMINARY; PRT; 17 AA.

DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE LDR dan (Fragment).

OS Mus musculus (Mouse).

OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;

RN [1] SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J;

RA Guenet J.-L.;"Characterization of an insertional mutation responsible for abnormal limb development."

RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RL EMBL; AF247636; AAL36969.1; -.

FT NON-TER 17 17

SQ SEQUENCE 17 AA; 1967 MW; E09EC2E5FFA554AA CRC64;

Query Match Similarity 24.7%; Score 22; DB 11; Length 17; Best Local Similarity 36.4%; Pred. No. 4.5e+03; 2; Mismatches 3; Indels 2; Gaps 1;

Matches 4; Conservative 36.4%; 2; Mismatches 3; Indels 2; Gaps 1;

Qy 4 WGC--KGRIC 12
Db 5 WGALLGLGALIC 15

RESULT 29

Q93TWO PRELIMINARY; PRT; 20 AA.

ID Q93TWO; PRELIMINARY; PRT; 20 AA.

AC Q93TWO; PRELIMINARY; PRT; 20 AA.

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE Pilin glycosylation protein PgIC (Fragment).

GN PgIC.

OS Neisseria meningitidis.

OC Bacteric; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

OX NCBI_TaxID=487;

RN [1] SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RC STRAIN=RMB;

RX MEDLINE=21246556; PubMed=11349019;

RA Kahlke C.M., Martin L.E., Tzeng Y.L., Miller Y.K., Sharkey K., Stephens D.S., Davies J.K.;"Glycosylation Locus of Neisseria meningitidis Expressing Class II Pilin;" Infect. Immun. 69:3597-3604(2001).

RA Stephens D.S., Davies J.K.; Glycosylation Locus of Neisseria meningitidis Expressing Class II Pilin;" Infect. Immun. 69:3597-3604(2001).

RT "Polymorphisms in Pilin Glycosylation Locus of Neisseria meningitidis Expressing Class II Pilin;" Infect. Immun. 69:3597-3604(2001).

DR EMBL; AF320320; AAK56076.1; -.

FT NON-TER 20 20

SQ SEQUENCE 20 AA; 2239 MW; 5AAB734AA47D87FB CRC64;

Query Match Similarity 24.7%; Score 22; DB 2; Length 20; Best Local Similarity 50.0%; Pred. No. 5.3e+03; 2; Mismatches 2; Indels 0; Gaps 0;

Matches 3; Conservative 50.0%; 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LNSWQCG 6
Db 9 NSWNSLG 15

Db 6 LSPWPC 11

RESULT 30
 066202 PRELIMINARY; PRT; 12 AA.
 ID 066202; 072765;
 AC 066202; 072765;
 DT 01-NOV-1995 (TREMBREL. 01, Created)
 DT 01-NOV-1996 (TREMBREL. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBREL. 21, Last annotation update)
 DE Nucleocapsid protein (Fragment).
 OS Transmissible gastroenteritis virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
 OC Coronaviridae; Coronavirus.
 OX NCBI_TaxID=1149;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PURDUE-115;
 RX MEDLINE=8722415; PubMed=3035066;
 RA Laude H., Rascchaert D., Huet J.C.;
 RT "Sequence and N-terminal processing of the transmembrane protein EI of
 the coronavirus transmissible gastroenteritis virus.";
 RL J. Gen. Virol. 68:1687-1693(1987).
 DR EMBL: X05598; CAA29092.1;
 KW Nucleocapsid.
 FT NON_TER 12 12
 SEQUENCE 12 AA: 1348 MW: 35A1C5F9BD416D8 CRC64:
 SQ Query Match 23.6%; Score 21; DB 12; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.7e-03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SWG 5
 DB 9 SWG 11

Search completed: June 5, 2003, 09:00:37
 Job time : 30 secs

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				Gencore version 5.1.6
Copyright (c) 1993 - 2003	Compugen Ltd.			
Run on:	June 5, 2003, 08:58:39	Search time 34 Seconds		
Scoring table:	BLOSUM62	(without alignments)		
	Gapop 10.0	Gapext 0.5		
Searched:	908470 seqs, 133250620 residues	58.787 Million cell updates/sec		
Minimum DB seq length:	0			
Maximum DB seq length:	20			
Post-processing: Minimum Match 0%				
Database :	A-Geneseq_101021*			
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2:	/SIDS2/gcadata/geneseq/geneseq-emb1/AA1981.DAT:*			
3:	/SIDS2/gcadata/geneseq/geneseq-emb1/AA1982.DAT:*			
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22:	/SIDS2/gcadata/geneseq/geneseq-emb1/AA2001.DAT:*			
23:	/SIDS2/gcadata/geneseq/geneseq-emb1/AA2002.DAT:*			
Pred. No.	is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
		SUMMARIES		
Result No.	Score	Query Length	DB ID	Description
1	86	96.6	16 19	AAW0468
2	86	96.6	17 19	AAW0467
3	81	91.0	16 19	AAW0467
4	77	86.5	16 21	AAV79852
5	77	86.5	20 21	AAV79852
6	75	84.3	16 21	AAV79848
7	75	84.3	16 21	AAV79851
8	74	83.1	16 21	AAV79845
9	72	80.9	15 17	AAV08258
10	72	80.9	15 17	AAV03053
11	72	80.9	15 17	AAR88790
12	72	80.9	15 19	AAW14405
13	72	80.9	15 19	AAW17240
14	72	80.9	16 20	AAW23330
15	72	80.9	16 21	AAY79842
16	72	80.9	16 21	AAY79845
17	72	80.9	16 21	AAY79847
18	72	80.9	16 21	AAY79858
19	70	78.7	15 16	AAY79854
20	70	78.7	16 21	AAY79857
21	69	77.5	16 21	AAY79841
22	69	77.5	21 21	AYV79850
23	69	77.5	20 18	AAW4680
24	68	76.4	16 21	AYV79849
25	68	76.4	17 21	AAY76508
26	68	76.4	19 18	AAW4681
27	68	76.4	19 18	AAW6381
28	67	75.3	15 21	AYV79853
29	66	74.2	16 21	AYV79844
30	65	73.0	16 21	AYV79843
31	65	73.0	17 20	AAY5591
32	64	71.9	16 21	AYV79856
33	64	71.9	17 21	AYV79828
34	64	71.9	21 21	AAY76518
35	63	70.8	15 21	AYV79855
36	63	70.8	19 18	AAW6380
37	62	69.7	16 21	AYV79829
38	60	67.4	17 21	AAW6379
39	59	66.3	19 18	AAW6379
40	58	65.2	10 20	AAY5593
41	58	65.2	13 19	AAZ2196
42	58	65.2	19 11	AAR6326
43	57	64.0	19 16	AAY74578
44	57	64.0	19 17	AAW4219
45	57	64.0	20 18	AAW55484
46	56	62.9	12 20	AAY5598
47	56	62.9	15 20	AYV5592
48	56	62.9	17 11	AAR6056
49	55	61.8	16 16	AAY7242
50	55	61.8	15 20	AAW2328
51	55	61.8	16 20	AAW2329
52	55	61.8	16 23	ABY76500
53	55	61.8	17 11	AAR6049
54	55	61.8	17 11	AAR6057
55	55	61.8	17 11	AAR6073
56	55	61.8	17 16	AAR76722
57	55	61.8	19 19	AAW3335
58	54	60.7	11 20	AAY05594
59	54	60.7	14 16	AAR76726
60	60	60.7	14 19	AAW7241
61	61	60.7	14 19	AAY79820
62	62	60.7	14 23	ABY76498
63	63	60.7	15 15	AAW07191
64	64	60.7	16 20	AAW2323
65	65	60.7	16 20	AAR7324
66	66	60.7	16 20	AAW2325
67	67	60.7	17 11	AAR6048
68	68	60.7	17 11	AAR6071
69	69	60.7	17 11	AAR6072
70	70	60.7	17 11	AAR6072
71	71	60.7	17 17	AAR6089
72	72	60.7	18 11	AAW03340
73	73	60.7	18 23	ABY76499
74	74	60.7	19 11	AAY05143
75	75	60.7	19 18	AAN44677
76	76	60.7	19 18	AAN76382
77	77	60.7	20 11	AAR05156
78	78	60.7	20 17	AAN04232
79	79	60.7	12 14	AAY41602
80	80	59.6	12 17	AAB76157
81	81	59.6	12 17	AAR33063
82	82	59.6	14 11	AAR3967
83	83	59.6	14 11	AAP80178

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Score Match Length DB ID

Description

1: HIV-1 subtype O gp

2: HIV-1 subtype #8. S

3: HIV subtype 0 gp41

4: HIV subtype O (A)

5: HIV infection date

6: HIV infection date

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84 53 59.6 15 9 AAP80217
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 89 53 59.6 17 9 AAP80183
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 95 53 59.6 17 11 AAP80604
 96 53 59.6 17 11 AAP80655
 97 53 59.6 17 11 AAP80667
 98 53 59.6 18 12 AAR14442
 99 53 59.6 19 12 AAP80179
 100 53 59.6 19 9 AAP80218

ALIGNMENTS

RESULT 1
 AAW80468
 ID AAW80468 standard; peptide; 16 AA.
 XX
 AC AAW80468;
 XX
 DT 28-JAN-1999 (first entry)
 DE Peptide derived from a conserved sequence of group O human HIV.
 KW Group O human immune deficiency virus; HIV; detection; infection.
 XX
 OS Synthetic.
 OS Immune deficiency virus.
 XX
 PN WO9845323-A1.
 XX
 PD 15-OCT-1998.
 XX
 PR 06-APR-1998; 98WO-FR00691.
 XX
 PR 24-FEB-1998; 98FR-0002212.
 XX
 PR 09-APR-1997; 97FR-0004356.
 XX
 PA (SNFI) PASTEUR SANOFI DIAGNOSTICS SA.
 XX
 PI Chenebaux DMB, Delagneau JFH, Gadeille SJX, Rieunier FV;
 XX
 DR WPI; 1998-583190/49.
 XX
 PT New synthetic peptide(s) - useful for, e.g. detecting infection by
 PT human immune deficiency virus of group O
 XX
 PS Claim 6; Page 45; 55pp; French.
 XX
 AAW80459-74 represent synthetic peptides (either linear or cyclised by
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences
 CC connected around short highly conserved sequences present in isolates
 CC of group O human immune deficiency virus (HIV). The peptides are
 CC useful as immunological reagents for detecting infection by group O
 CC human immune deficiency virus (HIV).
 XX
 SQ Sequence 17 AA;
 Query Match 96.6%; Score 86; DB 19; Length 17;
 Best Local Similarity 86.7%; Pred. No. 2.6e-06;
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNSWCKGRICYVS 15
 DB 2 LNSWCKGRILVCYVS 16

RESULT 3
 AAW80467
 ID AAW80467 standard; peptide; 16 AA.
 XX
 AC AAW80467;
 XX
 DT 28-JAN-1999 (first entry)
 DE Peptide derived from a conserved sequence of group O human HIV.
 XX
 KW Group O human immune deficiency virus; HIV; detection; infection.
 XX
 OS Synthetic.
 OS Immune deficiency virus.
 XX
 PN WO9845323-A1.
 XX
 PD 15-OCT-1998.

Query Match 96.6%; Score 86; DB 19; Length 16;
 Best Local Similarity 86.7%; Pred. No. 2.4e-06;
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNSWCKGRICYTS 15
 DB 2 LNSWCKGRILVCYTS 16

PF 06-APR-1998; 98WO-FR00691.
 XX PR 24-FEB-1998; 98FR-0002212.
 PR 09-APR-1997; 97FR-0004356.
 XX PA (SNFI) PASTEUR SANOFI DIAGNOSTICS SA.
 PI Chenebaux DMB, Delagneau JFH, Gadelle STX, Rieunier FY;
 XX DR WPI; 1998-583190/49.
 XX PT New synthetic peptide(s) " useful for, e.g., detecting infection by
 PR human immune deficiency virus of group O
 XX PS Claim 6; Page 43; 55pp; French.
 XX CC AAW80459-74 represent synthetic peptides (either linear or cyclised by
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences
 CC connected around short highly conserved sequences present in isolates
 CC of group O human immune deficiency virus (HIV). The peptides are useful as immunological reagents for detecting infection by group O
 CC human immune deficiency virus (HIV).
 XX SQ Sequence 16 AA:
 Query Match 91.0%; Score 81; DB 19; Length 16;
 Best Local Similarity 80.0%; Pred. No. 1.4e-05; Indels 0; Gaps 0;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 YY OY 1 LNSWGCKGRICYTS 15
 DB 2 LSSWGCKGRILVCYTS 16
 RESULT 4
 ID AAY79852
 ID AAY79852 standard; Peptide; 16 AA.
 AC AAY79852;
 XX DT 10-MAY-2000 (first entry)
 DE HIV-1 group O env epitope, SEQ ID NO:112.
 DE HIV infection detection peptide SEQ ID NO:90.
 DE Varicella zoster virus; HIV; HIV-; detection; diagnosis; infection;
 DE viral chimeric peptide; therapy; immunological.
 DE Unidentified.
 DE OS
 PN WO200001719-A2.
 XX PD 13-JAN-2000.
 XX PT 02-JUL-1999; 99WO-US15114.
 XX PR 02-JUL-1998; 98US-0091659.
 XX PR 16-OCT-1998; 98US-0104685.
 XX PR 11-DEC-1998; 98US-0112026.
 XX PA (PEPT-) PEPTIDE SOLUTIONS.
 PI Chowdhury AM, Bernstein D, Kozhich A, Motsenbocker M;
 PT WPI; 2000-171000/15.
 XX PT Novel monoclonal antibodies useful as positive control reagent for
 PT detecting human immunodeficiency virus infections and diagnosing,
 PT evaluating or prognosis viral disease -
 XX PS Claim 20; Page 70; 148pp; English.
 XX The invention relates to anti-HIV-1 group O monoclonal antibodies, which
 CC may be used as positive control reagents in immunoassays to detect and
 CC differentiate HIV-1 infections. The invention also encompasses a
 CC monoclonal antibody which binds specifically to an HIV-1 group O
 CC antigen, which has no more than 15% cross reactivity to a corresponding
 CC antigen selected from HIV-1 group M antigens and HIV-2 antigens; and a
 CC method of using a monoclonal antibody as a positive control reagent in
 an immunoassay for the detection of anti HIV-1 group O antibodies. The
 CC monoclonal antibodies are useful as positive control reagents in
 CC immunoassays capable of detecting anti-HIV-1 group O antibodies. Such
 CC immunoassays involve coupling a monoclonal antibody with HIV group-1
 CC antigen and detecting the antigen-antibody complex. The monoclonal
 CC antibodies of the invention would be used to ensure that the reagents
 CC provided to detect HIV-1 group O antibody were performing properly. The
 CC monoclonal antibodies may also can be immobilized on a matrix and used
 CC for affinity purification of specific HIV-1 group O-derived proteins.
 CC

CC from cell cultures or biological tissues. The monoclonal antibodies can
 CC also be used for generating chimeric antibodies for therapeutic use.
 CC different synthetic, recombinant or purified antibodies which identify
 CC different epitopes of HIV antigens can be used in combination in assay to
 CC diagnose, evaluate, or prognosticate HIV disease condition. The
 CC monoclonal antibodies are also useful for differentiating HIV-1 Group O
 CC antigens from HIV-group M and HIV-2 antigens. Sequences AAY77389-Y77398
 CC represent HIV-1 group O env epitopes.

SQ Sequence 20 AA;

Query Match 86.5%; Score 77; DB 21; Length 20;
 Best Local Similarity 85.7%; Pred. No. 6.7e-05; 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

RESULT 6
 AAY79848

ID AAY79848 standard; Peptide; 16 AA.

XX XX

AC AC

XX XX

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

XX XX

AC AC

XX XX

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

XX XX

AC AC

XX XX

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

XX XX

AC AC

XX XX

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

XX XX

AC AC

XX XX

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

XX XX

AC AC

XX XX

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

XX XX

AC AC

XX XX

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

XX XX

AC AC

XX XX

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

XX XX

AC AC

XX XX

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

XX XX

AC AC

XX XX

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

XX XX

AC AC

XX XX

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

XX XX

AC AC

XX XX

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

XX XX

AC AC

XX XX

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

XX XX

AC AC

XX XX

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

XX XX

AC AC

XX XX

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

XX XX

AC AC

XX XX

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

XX XX

AC AC

XX XX

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

XX XX

AC AC

XX XX

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

XX XX

AC AC

XX XX

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

XX XX

AC AC

XX XX

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

XX XX

AC AC

XX XX

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

XX XX

AC AC

XX XX

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

XX XX

AC AC

XX XX

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

XX XX

AC AC

XX XX

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

XX XX

AC AC

XX XX

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

XX XX

AC AC

XX XX

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

XX XX

AC AC

XX XX

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

XX XX

AC AC

XX XX

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

XX XX

AC AC

XX XX

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

XX XX

AC AC

XX XX

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

XX XX

AC AC

XX XX

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

XX XX

AC AC

XX XX

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

XX XX

AC AC

XX XX

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

XX XX

AC AC

XX XX

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

XX XX

AC AC

XX XX

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

XX XX

AC AC

XX XX

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

XX XX

AC AC

XX XX

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

XX XX

AC AC

XX XX

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

Db 1 LNSWGAGRKVCTS 15

XX XX

AC AC

XX XX

QY 1 LNSWGCKGRICYTS 15
 ||||| || :||| 15

KW Varicella zoster virus; HIV; HIV-2; detection; diagnosis; infection;
 KW viral chimeric peptide; therapy; immunological.
 XX
 OS Unidentified.
 XX
 PN WO200001719-A2.
 PD 13-JAN-2000.
 XX
 PF 02-JUL-1999; 99WO-US15114.
 XX
 PR 02-JUL-1998; 98US-0091659.
 PR 16-OCT-1998; 98US-0104685.
 PR 11-DEC-1998; 98US-0112026.
 XX
 PA (PEPT-) PEPTIDE SOLUTIONS.
 XX
 PI Chowdhury AM, Bernstein D, Kozhich A, Motsenbocker M;
 DR XX
 WPI: 2000-171000/15.
 XX
 PT Novel viral-derived peptides used for the detection of human
 immunodeficiency virus (HIV) infection, particularly HIV-2 infection -
 XX
 PS Disclosure; Fig 1; 67pp; English.
 XX
 CC The present invention describes a peptide (I) for detecting HIV-2
 CC infection, which comprises a core Varicella-Zoster protein 51 sequence,
 CC also described in the present invention are methods for detecting HIV
 CC infection. Peptides from the present invention can be used for the
 CC immunological detection of anti-HIV antibody, particularly for HIV-2
 CC testing. The peptides have high sensitivity and selectivity for HIV.
 CC The improved peptides have increased stability and selectivity which allows the
 CC peptides to react more favourably to give more sensitive tests. AAY7976-
 CC present invention.
 XX
 SQ Sequence 16 AA;
 XX
 Query Match 83.1%; Score 74; DB 21; Length 16;
 Best Local Similarity 66.7%; Pred. No. 0.00015; Gaps
 Matches 10; Conservative 4; Mismatches 1; Indels 0;
 QY 1 LNSWGCGRGTCITS 15
 1 ||:||| |:::|||
 Db 1 LNAWCAGKLVCITS 15
 XX
 RESULT 9
 AAY08268
 ID AAY08268 standard; peptide: 15 AA.
 XX
 AC AAY08268;
 XX
 DT 13-JUL-1999 (first entry)
 XX
 DE HTV 1 subtype O gp41 epitope 2.
 XX
 KW Epitope; immunological detection; antibody; solid phase; antigen;
 KW pathogenic organism; bacteria; virus; protozoa; autoimmune antigen;
 KW seroconversion; sensitivity; gp120; gp41; gp32; NS5; NS4; NS3.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 PN DE4430972-A1.
 PD 01-FEB-1996.
 XX
 PF 31-AUG-1994; 94DE-4430972.
 XX
 PR 25-JUL-1994; 94DE-4426276.
 XX
 PA (BOEFE) BOHRINGER MANNHEIM GMBH

XX
 PI Faatz E, Hoess E, Kruse-Muller C, Ofenloch-Hahne B;
 PI Seidel C, Wiedemann M, Wienhues-Thelen U;
 XX
 XX
 PT Immunooassay of specific antibodies using two antigens - one labelled
 PT and the other bound to solid phase, with at least one having
 PT multiple epitopes recognised by the antibody to improve sensitivity.
 XX
 PS Disclosure; Page 22; 30pp; German.
 XX
 CC This invention describes a method for the immunological detection of
 CC an antibody which comprises incubating a test sample, in presence of a
 CC solid phase, with 2 antigens directed against the antibody, one antigen
 CC (Ag1) carrying a label and the other (Ag2) being either bound to the
 CC solid phase or bindable to it. The antibody is detected from measurement
 CC of the label in the solid and/or liquid phases. The new feature is that
 CC at least one antigen comprises multiple epitope regions reactive with
 CC antibody. The method is used to detect antibodies related to pathogenic
 CC organisms (bacteria, viruses or protozoa) or autoimmune antigens,
 CC especially antibodies against HIV or hepatitis C. The method can detect
 CC antibodies even very shortly after seroconversion and in cases where new
 CC microbial subtypes are involved. The use of multiple epitopes improves
 CC sensitivity (especially for low affinity antibodies) and significantly
 CC reduces the risk of false negatives from high titre samples caused by
 CC the hook effect. Multimeric antigens are also more stable than monomeric
 CC antigens. AAY08261-Y08276 are epitopes used in the method of the
 XX invention.
 XX
 SQ Sequence 15 AA:
 XX
 Query Match 80.9%; Score 72; DB 17; Length 15;
 Best Local Similarity 66.7%; Pred. No. 0.00029;
 Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 XX
 QY 1 LNSWGCKGRICVYTS 15
 |:||||:|||
 -Db 1 LSLWGCKGKLVCYTS 15
 XX
 RESULT 10
 AAW03053
 ID AAW03053 standard; Peptide; 15 AA.
 XX
 AC AAW03053;
 XX
 DT 20-SEP-1996 (first entry)
 XX
 DE Epitope from gp41.
 XX
 KW HIV; epitope; haptens-labelled; immunoassay.
 XX
 OS Human immunodeficiency virus type 1, subtype O.
 XX
 PN DE4430973-A1.
 XX
 PD 01-FEB-1996.
 XX
 PF 31-AUG-1994; 94DE-4430973.
 XX
 PR 25-JUL-1994; 94DE-4426276.
 XX
 PA (BOEFL) BOEHRINGER MANNHEIM GMBH.
 XX
 PT Faatz E, Hoess E, Schmitt U, Seidel C, Wienhues-Thelen UH;
 XX
 DR WFI; 1996-130245/14.
 XX
 PT Prepn. of haptens-labelled peptide - by reacting haptens activated
 PT ester with selected peptide prim. amino gps., useful as reagents for
 PT detecting specific antibodies.

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PS	Claims 14, 21; Pages 21, 22; 23pp; German.
CC	New haptens-labelled peptides are claimed which consist of (1) a peptide of max. length 50 amino acids, and (2) a hapten attached to the peptide at the N-terminal or at a side chain amino group. The hapten is a steroid, bile acid, sex hormone, corticoid, cardenolide (or its glycoside), bisabolenolide, steroid-saponin or a steroid alkaloid. The labelled peptides are useful for immunological determination of antibodies against bacteria, viruses, protozoa or autoimmune antigens, etc., esp. antibodies against HIV or hepatitis C virus. The peptide consists of an immunologically reactive epitope region and a spacer region (of 1-10 amino acids which contain charged groups or groups able to form H-bonds). The present sequence represents a preferred epitope region which can be used in the labelled peptides.
CC	SO Sequence 15 AA;
CC	Query Match 80.9%; Score 72; DB 17; length 15;
CC	Best Local Similarity 66.7%; pred. No. 0 0029; 1; Indels 0; Gaps
CC	Matches 10; Conservative 4; Mismatches 1;
CC	QY 1 LINSWGCKGRICYTS 15
CC	Db 1 LSLWGSRKGVCYTS 15
XX	RESULT 11
XX	AAR88790
XX	ID AAR88790 standard; peptide; 15 AA.
XX	AC AAR88790;
XX	DT 01-OCT-1996 (first entry)
XX	DE HIV-1 subtype O gp41 epitope labelled by metal chelate.
XX	KW HIV-1; HIV-1; glycoprotein gp41; epitope; antigen; immunoassay;
XX	KW metal chelate-labelled.
OS	Human immunodeficiency virus type 1.
FR	Key Location/Qualifiers
FT	Modified-site 1.15
FT	/note= "at least one of N-terminus and/or side-chain amino groups is modified post-synthesis by coupling of an activated luminescent metal chelate (LMC) or at least one amino acid covalently coupled to a LMC is incorporated during peptide synthesis"
FT	DE4430998-A1.
XX	PN DE4430998-A1.
XX	PD 01-FEB-1996.
XX	PF 31-AUG-1994; 94DE-4430998.
XX	PR 25-JUL-1994; 94DE-4426276.
XX	PA (BOEFL) BOEHRINGER MANNHEIM GMBH.
XX	PT Seidel C., Roess E., Wienhues-Thelen U;
XX	DR WPI; 1996-130246/14.
PT	Prepn. of metal chelate labelled peptide(s) for use as antigens - in immunoassays of antibodies, by reacting activated chelate with prim. amino gps. in a peptide, also new chelate-contg. amino acids
XX	PS Claim 23; Page 19; 21pp; German.
CC	New metal chelate-labelled peptides are claimed which consist of (1) a peptide of max. length 50 amino acids, and (2) a luminescent metal chelate attached to the peptide at the N-terminal or at a side-
CC	PS

chain amino group. The chelates pref. contain Re, IR, OS or esp. Ru and the ligands are aromatic heterocyclic polydentate ligands such as bipyridyl, bipyrrazyl, terpyridyl or phenanthrolyl. The labelled peptides are useful for immunological determination of antibodies against bacteria, viruses, protozoa or autoimmune antigens, etc., esp. antibodies against HIV or hepatitis C virus. The peptide consists of an immunologically reactive epitope region and a spacer region (of 1-10 amino acids which contain charged groups or groups able to form H-bonds). The present sequence represents a preferred epitope region from HIV-1 subtype O which can be used in the labelled peptides.

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PR 16-OCT-1998; 98US-0104685.
 PR 11-DEC-1998; 98US-0112026.
 XX
 PA (PEPT-) PEPTIDE SOLUTIONS.
 XX
 PI Chowdhury AM, Bernstein D, Kozhich A, Motzenbocker M;
 DR WPI; 2000-171000/15.
 PT Novel viral-derived peptides used for the detection of human immunodeficiency virus (HIV) infection, particularly HIV-2 infection
 PT disclosure; Fig 1; 67pp; English.
 XX
 CC The present invention describes a peptide (I) for detecting HIV-2 infection, which comprises a core Varicella-Zoster protein 51 sequence, also described in the present invention are methods for detecting HIV infection. Peptides from the present invention can be used for the immunological detection of anti-HIV antibody, particularly for HIV-2 testing. The peptides have high sensitivity and selectivity for HIV.
 CC The improved peptides have increased stability which allows the peptides to react more favourably to give more sensitive tests. AAY79763 to AAY79868 represent peptides used in the exemplification of the present invention.
 CC
 XX Sequence 16 AA;
 SQ Query Match 78.7%; Score 70; DB 21; Length 16;
 Best Local Similarity 73.3%; Pred. No. 0.00061; Mismatches 11; Conservative 1; Indels 0; Gaps 0;
 Matches 11; DB 1 LNPWGCAGRCVCTS 15
 OY 1 LNSWGCKGRICVTS 15
 ||||| :||| :|||
 1 LNPWGCAGRCVCTS 15
 Db
 XX
 RESULT 21
 AAY79841
 ID AAY79841 standard; Peptide; 16 AA.
 XX
 AC AAY79841;
 XX
 DT 10-MAY-2000 (first entry)
 DE HIV infection detection peptide SEQ ID NO:79.
 DE HIV infection detection peptide SEQ ID NO:88.
 KW Varicella zoster virus; HIV; HIV-2; detection; diagnosis; infection;
 KW viral chimeric peptide; therapy; immunological.
 XX
 OS Unidentified.
 XX
 PN WO200001719-A2.
 XX
 PD 13-JAN-2000.
 XX
 PF 02-JUL-1999; 99WO-US15114.
 XX
 PR 02-JUL-1998; 98US-0091659.
 PR 16-OCT-1998; 98US-0104685.
 PR 11-DEC-1998; 98US-0112026.
 XX
 PA (PEPT-) PEPTIDE SOLUTIONS.
 XX
 PI Chowdhury AM, Bernstein D, Kozhich A, Motzenbocker M;
 DR WPI; 2000-171000/15.
 PT Novel viral-derived peptides used for the detection of human immunodeficiency virus (HIV) infection, particularly HIV-2 infection
 PT disclosure; Fig 1; 67pp; English.
 XX
 CC The present invention describes a peptide (I) for detecting HIV-2 infection, which comprises a core Varicella-Zoster protein 51 sequence, also described in the present invention are methods for detecting HIV infection. Peptides from the present invention can be used for the immunological detection of anti-HIV antibody, particularly for HIV-2 testing. The peptides have high sensitivity and selectivity for HIV. The improved peptides have increased stability which allows the peptides to react more favourably to give more sensitive tests. AAY79763 to AAY79868 represent peptides used in the exemplification of the present invention.
 CC
 XX Sequence 16 AA;
 SQ Query Match 77.5%; Score 69; DB 21; Length 16;
 Best Local Similarity 66.7%; Pred. No. 0.00086; Mismatches 11; Conservative 1; Indels 0; Gaps 0;
 Matches 10; DB 1 LNANGCAGKQVCTS 15
 OY 1 LNANGCAGKQVCTS 15
 ||:||| :||| :|||
 1 LNANGCAGKQVCTS 15
 Db
 XX
 RESULT 22
 AAY79850
 ID AAY79850 standard; Peptide; 16 AA.
 XX
 AC AAY79850;
 XX
 DT 10-MAY-2000 (first entry)
 DE HIV infection detection peptide SEQ ID NO:88.
 DE HIV infection detection peptide SEQ ID NO:88.
 KW Varicella zoster virus; HIV; HIV-2; detection; diagnosis; infection;
 KW viral chimeric peptide; therapy; immunological.
 XX
 OS Unidentified.
 XX
 PN WO200001719-A2.
 XX
 PD 13-JAN-2000.
 XX
 PF 02-JUL-1999; 99WO-US15114.
 XX
 PR 02-JUL-1998; 98US-0091659.
 PR 16-OCT-1998; 98US-0104685.
 PR 11-DEC-1998; 98US-0112026.
 XX
 PA (PEPT-) PEPTIDE SOLUTIONS.
 XX
 PI Chowdhury AM, Bernstein D, Kozhich A, Motzenbocker M;
 DR WPI; 2000-171000/15.
 PT Novel viral-derived peptides used for the detection of human immunodeficiency virus (HIV) infection, particularly HIV-2 infection
 PT disclosure; Fig 1; 67pp; English.
 XX
 CC The present invention describes a peptide (I) for detecting HIV-2 infection, which comprises a core Varicella-Zoster protein 51 sequence, also described in the present invention are methods for detecting HIV infection. Peptides from the present invention can be used for the immunological detection of anti-HIV antibody, particularly for HIV-2 testing. The peptides have high sensitivity and selectivity for HIV. The improved peptides have increased stability which allows the peptides to react more favourably to give more sensitive tests. AAY79763 to AAY79868 represent peptides used in the exemplification of the present invention.
 CC
 XX Sequence 16 AA;
 SQ Query Match 77.5%; Score 69; DB 21; Length 16;
 Best Local Similarity 73.3%; Pred. No. 0.00086; Mismatches 11; Conservative 1; Indels 0; Gaps 0;
 Matches 10; DB 1 LNANGCAGKQVCTS 15
 OY 1 LNANGCAGKQVCTS 15
 ||:||| :||| :|||
 1 LNANGCAGKQVCTS 15
 Db
 XX
 RESULT 23
 AAY79868
 ID AAY79868 standard; Peptide; 16 AA.
 XX
 AC AAY79868;
 XX
 DT 10-MAY-2000 (first entry)
 DE HIV infection detection peptide SEQ ID NO:88.
 DE HIV infection detection peptide SEQ ID NO:88.
 KW Varicella zoster virus; HIV; HIV-2; detection; diagnosis; infection;
 KW viral chimeric peptide; therapy; immunological.
 XX
 OS Unidentified.
 XX
 PN WO200001719-A2.
 XX
 PD 13-JAN-2000.
 XX
 PF 02-JUL-1999; 99WO-US15114.
 XX
 PR 02-JUL-1998; 98US-0091659.
 PR 16-OCT-1998; 98US-0104685.
 PR 11-DEC-1998; 98US-0112026.
 XX
 PA (PEPT-) PEPTIDE SOLUTIONS.
 XX
 PI Chowdhury AM, Bernstein D, Kozhich A, Motzenbocker M;
 DR WPI; 2000-171000/15.
 PT Novel viral-derived peptides used for the detection of human immunodeficiency virus (HIV) infection, particularly HIV-2 infection
 PT disclosure; Fig 1; 67pp; English.
 XX
 CC The present invention describes a peptide (I) for detecting HIV-2 infection, which comprises a core Varicella-Zoster protein 51 sequence, also described in the present invention are methods for detecting HIV infection. Peptides from the present invention can be used for the immunological detection of anti-HIV antibody, particularly for HIV-2 testing. The peptides have high sensitivity and selectivity for HIV. The improved peptides have increased stability which allows the peptides to react more favourably to give more sensitive tests. AAY79763 to AAY79868 represent peptides used in the exemplification of the present invention.
 CC
 XX Sequence 16 AA;

RESULT 23	1	LNSWGCKGRICIVTS	15
ID	ID	AYY79849	standard; Peptide; 16 AA.
Db	1	LNSWGCAQRQVCYTS	15
XX	XX	XX	XX
AC	AC	AYY79849;	
XX	XX	XX	XX
XX	XX	XX	XX
DT	10-MAY-1998	(first entry)	
XX	XX	XX	XX
DE	HIV infection detection peptide SEQ ID NO:87.		
XX	XX	XX	XX
KW	Varicella zoster virus; HIV; HIV-2; detection; diagnosis; infection;		
KW	viral chimeric peptide; therapy; immunological.		
KW	OS	unidentified.	
XX	XX	XX	XX
DE	HIV infection detection peptide SEQ ID NO:87.		
XX	XX	XX	XX
KW	Varicella zoster virus; HIV; HIV-2; detection; diagnosis; infection;		
KW	viral chimeric peptide; therapy; immunological.		
XX	XX	XX	XX
DT	10-MAY-2000	(first entry)	
XX	XX	XX	XX
DE	HIV infection detection peptide SEQ ID NO:87.		
XX	XX	XX	XX
KW	Varicella zoster virus; HIV; HIV-2; detection; diagnosis; infection;		
KW	viral chimeric peptide; therapy; immunological.		
XX	XX	XX	XX
OS	unidentified.		
XX	XX	XX	XX
DE	HIV infection detection peptide SEQ ID NO:87.		
XX	XX	XX	XX
KW	Varicella zoster virus; HIV; HIV-2; detection; diagnosis; infection;		
KW	viral chimeric peptide; therapy; immunological.		
XX	XX	XX	XX
DT	01-MAY-1998	(first entry)	
XX	XX	XX	XX
DE	Haptien-peptide conjugate #4 to detect anti-HIV-1 antibodies.		
XX	XX	XX	XX
KW	Haptien-peptide; HIV; immunoassay; detection; antibody; HIV-1;		
KW	capture reagent; haptienised peptide; HIV-2.		
XX	XX	XX	XX
OS	Syntetic.		
OS	Human immunodeficiency virus type 1.		
XX	XX	XX	XX
Key	Location/Qualifiers		
FT	Modified-site.		
FT	1		
FT	/note= "Alpha amino group of Lys1 is optionally modified		
FT	by biotin-amidocaproyl"		
XX	XX	XX	XX
XX	XX	XX	XX
PN	WO961187-A1.		
XX	XX	XX	XX
PD	19-DEC-1996.		
XX	XX	XX	XX
PF	07-JUN-1996;	96WO-US09507.	
XX	XX	XX	XX
PR	07-JUN-1995;	95US-0486657.	
XX	XX	XX	XX
PA	(ABBO) ABBOTT LAB.		
XX	XX	XX	XX
PT	Briddon DP, Chang C, Colpitts TL, Daghfal DJ, Jaffe K;		
PT	Merchant BT, Sze I;		
PR	WPI; 1997-108656/10.		
XX	XX	XX	XX
XX	XX	XX	XX
PT	Immunassay for HIV specific antibody detection - uses peptide		
PT	haptienised at N terminus for reaction with the initial complex of		
PT	antibody and capture reagent		
XX	XX	XX	XX
PS	Claim 1; Page 8; 37pp; English.		
XX	XX	XX	XX
CC	This sequence represents a peptide derived from the human immuno-		
CC	deficiency virus-1 (HIV-1) gp41, type 0. N-terminal haptienised peptides		
CC	AAW4677-82 are used in an improved immunoassay for detecting anti-HIV-1		
CC	or -2 antibodies (Ab). The method comprises: (i) reacting sample with		
CC	capture reagent (CR) to form a CR-Ab complex (C); (ii) treating this		
CC	complex with a haptienised peptide conjugate (CJ) to form a C-CJ complex;		
CC	(iii) treating this with an indicator (I) to form a C-CJ-I complex; and		
CC	(iv) detecting a signal generated from I. The haptien is attached at a		
CC	known, predetermined position, outside the epitope so that it cannot		
CC	interfere with binding to antibody. This provides a better assay than		
CC	similar peptides haptienised randomly in solution.		
SO	Sequence 20 AA;		
SO	Sequence 16 AA;		
Query Match	77.5%	Score 69; DB 18; Length 20;	
Best Local Similarity	71.4%	Pred. No. 0.00112; Length 16;	
Matches	10;	Conservative 1; Mismatches 3; Indels 0; Gaps 0;	
Db	1	LNSWGCKGRICIVTS 15	
QY	1	LNSWGCKGRICIVTS 15	
QY	1	:	
Db	1	LNSWGCAQRQVCYTS 15	
XX	XX	XX	XX
AC	AYY7608;		
AC	AYY7608;		
AC	AYY7608 standard; Peptide; 17 AA.		
XX	XX	XX	XX
DT	23-MAR-2000 (first entry)		
XX	XX	XX	XX
DE	Peptide #8 for detecting HIV-1 group O infection.		
XX	XX	XX	XX
KW	Human immunodeficiency virus-1; HIV-1; gp41 envelope protein; detection;		
KW	increased structural stability; diagnostic antigen.		
XX	XX	XX	XX
OS	Syntetic.		
XX	XX	XX	XX
FH	Key		
FH	Location/Qualifiers		

FT /note- "mutated from Ser residue in wild type
 FT sequence (AMW16382)"
 FT Misc-difference 18 /note- "mutated from Thr residue in wild type
 FT sequence (AMW16382)"
 XX WO9640763-A2.
 XX PD 19-DEC-1996.
 XX PF 07-JUN-1996; 96WO-US09655.
 XX PR 07-JUN-1995; 95US-0472597.
 XX PA (ABBO) ABBOTT LAB.
 XX PT Bridon DP, Colpitts TL, Daghfal DJ, Jaffe RD, Sze IS;
 XX DR WPI; 1997-052229/05.
 PT Hybrid polypeptide(s) comprising HIV-1 sub-type B immuno-dominant region - contg. 1 or more specific amino acid substitutions critical for detecting HIV-1 sub-type O, useful in immunoassay for detecting HIV antibodies
 XX PS Claim 12; Page 25; 34pp; English.
 CC The polypeptides AMW16379-81 represent peptides having point mutations in the HIV-1 sub-type B immunodominant region (IDR) at positions 604 and/or 610. The peptides correspond to residues 593-611 of the gp41 protein. This peptide has point mutations at positions 604 and 610. The invention relates to polypeptides which are hybrid polypeptides comprising the gp41 IDR or HIV-1 sub-type B contg. 1 or more specific amino acid substitutions critical for the detection of HIV-1 sub-type O. The polypeptides can be used for the detection of HIV antibodies.
 XX SQ Sequence 19 AA:
 Query Match 76.4%; Score 68; DB 18; Length 19;
 Best Local Similarity 71.4%; Pred. No. 0.0014; Mismatches 2; Indels 0; Gaps 0;
 Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 CC Oy 1 LNSWQCKGRICYT 14
 CC 2 |||||:|||||
 CC Db 6 LGIWCQCKGRICYT 19
 RESULT 28
 ID AAY79853 standard; Peptide: 16 AA.
 ID AAY79853 standard; Peptide: 16 AA.
 ID AAY79853;
 AC XX
 DT 10-MAY-2000 (first entry)
 DE HIV infection detection Peptide SEQ ID NO:82.
 XX KW Varicella zoster virus; HIV; HIV-2; detection; diagnosis; infection;
 XX KW viral chimeric peptide; therapy; immunological.
 OS Unidentified.
 XX PN WO200001719-A2.
 XX PD 13-JAN-2000.
 XX PF 02-JUL-1999; 99WO-US15114.
 XX PR 02-JUL-1998; 98US-0091659.
 PR 16-OCT-1998; 98US-0104655.
 PR 11-DEC-1998; 98US-0112026.
 XX PA (PEPT-) PEPTIDE SOLUTIONS.
 PT Chowdhury AM, Bernstein D, Kozhich A, Motsenbocker M;
 DR WPI; 2000-171000/15.
 XX Novel viral-derived peptides used for the detection of human
 PT immunodeficiency virus (HIV) infection, particularly HIV-2 infection -
 XX Disclosure; Fig 1; 67pp; English.
 XX The present invention describes a peptide (1) for detecting HIV-2
 CC infection, which comprises a core Varicella-Zoster protein 51 sequence.
 CC also described in the present invention are methods for detecting HIV
 CC infection. Peptides from the present invention can be used for the
 immunological detection of anti-HIV antibody, particularly for HIV-2
 CC immunological detection of anti-HIV antibody, particularly for HIV-2

CC testing. The peptides have high sensitivity and selectivity for HIV.
 CC The improved peptides have increased stability which allows the
 CC peptides to react more favourably to give more sensitive tests. AAY79763
 CC to AAY79868 represent peptides used in the exemplification of the
 CC present invention.

XX Sequence 16 AA;

Query Match 74.2%; Score 66; DB 21; Length 16;

Best Local Similarity 66.7%; Pred. No. 0.0024; Mismatches 3; Indels 0; Gaps 0;

Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LNSWGCKGRICYTS 15
 1 ||:||| | :|||

Db 1 LNAWGCANRQVCYTS 15

RESULT 30
 AAY79843
 ID AAY79843 standard; Peptide: 16 AA.

XX
 AC AAY79843;

XX
 DT 10-MAY-2000 (first entry)

XX DE HIV infection detection peptide SEQ ID NO:81.

XX Varicella zoster virus; HIV; HIV-2; detection; diagnosis; infection;

XX viral chimeric peptide; therapy; immunological; Unidentified.

XX OS Unidentified.

XX PN WO200001719-A2.

XX PD 13-JAN-2000.

XX PF 02-JUL-1999; 99WO-US15114.

XX PR 02-JUL-1998; 98US-0091659.

XX PR 16-OCT-1998; 98US-0104685.

XX PR 11-DEC-1998; 98US-0112026.

XX (PEPT-) PEPTIDE SOLUTIONS.

XX Chowdhury AM, Bernstein D, Kozhich A, Motsenbocker M;

PT XX

DR XX

WPI; 2000-171000/15.

XX Novel viral-derived peptides used for the detection of human immunodeficiency virus (HIV) infection, particularly HIV-2 infection

XX Disclosure; Fig 1; 67pp; English.

XX The present invention describes a peptide (I) for detecting HIV-2 infection, which comprises a core Varicella-Zoster protein 51 sequence. CC The improved peptides used in the exemplification of the present invention are methods for detecting HIV also described in the present invention. Peptides from the present invention can be used for the CC detection of anti-HIV antibody, particularly for HIV-2 immunological detection of anti-HIV antibody, particularly for HIV-2 testing. The peptides have high sensitivity and selectivity for HIV. CC The improved peptides have increased stability which allows the CC peptides to react more favourably to give more sensitive tests. AAY79763 CC to AAY79868 represent peptides used in the exemplification of the CC present invention.

XX Sequence 16 AA;

Query Match 73.0%; Score 65; DB 21; Length 16;

Best Local Similarity 66.7%; Pred. No. 0.0034; Mismatches 3; Indels 0; Gaps 0;

Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LNSWGCKGRICYTS 15
 1 ||:||| | :|||

Db 1 LNAWGCAQDRCYTS 15

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